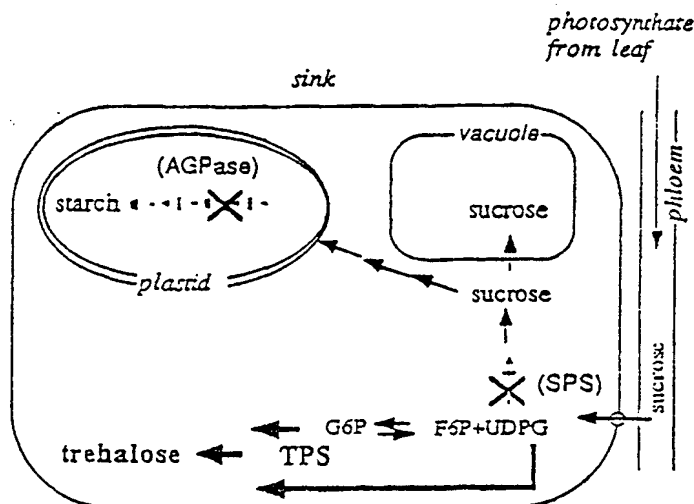




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(54) Title: PRODUCTION OF TREHALOSE IN PLANTS

ENGINEERING OF  
TREHALOSE-PRODUCTION  
IN PLANTS

## (57) Abstract

The present invention provides for the production of trehalose in a plant host due to the presence in said plant host of a plant expressible gene which comprises in sequence: a) a transcriptional initiation region that is functional in said plant host, b) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally c) a transcriptional termination sequence that is functional in said plant host.

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## PRODUCTION OF TREHALOSE IN PLANTS

## FIELD OF THE INVENTION

This invention relates to the modification of plant carbohydrate metabolism using recombinant DNA techniques, recombinant DNA for use therein, as well as plants and parts of plants having a modified genetic constitution. Said plants may be used to extract specific carbohydrate compounds, or alternatively, they may be processed as food, feed, or ingredients thereof, having improved properties due to the presence of said carbohydrate compounds, e.g. during processing.

## STATE OF THE ART

Trehalose is a general name given to D-glucosyl D-glucosides which comprise disaccharides based on two  $\alpha$ -,  $\alpha$ , $\beta$ - and  $\beta$ , $\beta$ -linked glucose molecules. Trehalose, and especially  $\alpha$ -trehalose 1-(O- $\alpha$ -D-glucopyranosyl)-1'-O- $\alpha$ -D-glucopyranose) is a widespread naturally occurring disaccharide.

The chemical synthesis of trehalose is difficult (protecting groups required) and inefficient. Current natural sources of trehalose are mushrooms and the yeast *Saccharomyces cerevisiae*, that can accumulate over 10% of dry weight as trehalose. However production is hampered by high trehalase activity causing rapid metabolization of trehalose. Elbein A.D. (1974, Adv. Carbohydrate Chem. and Biochem. 30, 227-256) gives a review of the occurrence and metabolism of the disaccharide trehalose, particularly  $\alpha$ , $\alpha$ -trehalose, in living organisms. In plants, the presence of trehalose has been reported in some lower plant species, as well as in a number of higher plant species belonging to the spermatophyta; Echinops persicus, Carex brunescens; Fagus sylvaticus. However, these results have never been firmly established by other authors (e.g. Kendall et al., 1990, Phytochemistry 29, No. 8, 2525-2528). For instance, Kendall et al, supra, referring to the occurrence of trehalose in spermatophytes, stated that the presence thereof has only been firmly documented for caraway seed (Carum carvi). A report of the presence of trehalose in sunflower by Cegla et al., (1977, J. Am. Oil Chem. Soc. 54, 150 et seq.) was questioned by Kandler et al., (in: The Biochemistry of Plants Vol. 3 Carbohydrates: Structure and Function; Preiss, J., ed., p.228. Academic

Press) according to Kendall et al, 1990, supra. Reports of trehalose in beech (Fagus sylvaticus) and cabbage could not be verified by other authors (Kendall et al., 1990, supra, and references therein).

In spite of the apparent rarity of trehalose in higher plants, the presence of trehalose degrading activities was reported for a significant number of the investigated plant families. Stable high trehalase activity was found in three wheat lines, jack pine, and Selaginella lepidophylla. Stable, low trehalase activity was found in alfalfa, black Mexican sweet corn and white spruce. Labile, moderate activities were found in two different suspensions of canola, but these could probably not be ascribed to specific trehalase activity. Barley, brome grass, soybean and black spruce were reported to contain no trehalase activity at all (Kendall, 1990, supra).

In organisms capable of its production, trehalose is believed to be biosynthesized as the 6-phosphate, whereas the storage form is the free sugar. It is therefore believed, that organisms that produce and/or store trehalose contain a phosphatase capable of cleaving trehalose 6-phosphate (Elbein, 1974, supra). Little is known about the presence of specific trehalose phosphate phosphatases in higher plants.

International patent application WO93/17093 A1, published on september 2, 1993, describes the production of trehalose in yeast transgenic for yeast genes coding for trehalose phosphate synthase. It was suggested that trehalose may be produced in higher plants as well, using these yeast genes, but there is no actual disclosure of trehalose production in a plant. It is to be noted that WO93/17093 A1 was published prior to the filing date but subsequent to the priority date of the instant application.

#### SUMMARY OF THE INVENTION

The present invention provides for a method for the production of trehalose in a plant host due to the presence in said plant host of a plant expressible gene which comprises in sequence:

- (a) a transcriptional initiation region that is functional in said plant host,
- (b) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally

(c) a transcriptional termination sequence that is functional in said plant host.

Another embodiment of the invention comprises the production of trehalose in a plant host due to the presence in said plant host of a plant expressible gene which comprises in sequence:

(d) a transcriptional initiation region that is functional in said plant host,

(e) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally

(f) a transcriptional termination sequence that is functional in said plant host, and

a plant expressible gene comprising in sequence:

(a) a transcriptional initiation region that is functional in said plant host,

(b) a DNA sequence encoding an RNA sequence which is at least partially complementary to an RNA sequence which encodes a sucrose phosphate synthase enzyme (SPS) naturally occurring in said plant host, and optionally

(c) a transcriptional termination sequence that is functional in said plant host.

Yet another embodiment of the invention comprises the production of trehalose in a plant host due to the presence in said plant host of a plant expressible gene which comprises in sequence:

(d) a transcriptional initiation region that is functional in said plant host,

(e) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally

(f) a transcriptional termination sequence that is functional in said plant host, and

a plant expressible gene comprising in sequence:

(a) a transcriptional initiation region that is functional in said plant host,

(b) a DNA sequence encoding an RNA sequence which is at least partially complementary to an RNA sequence which encodes an ADP-glucose pyrophosphorylase enzyme naturally occurring in said plant host, and optionally

(c) a transcriptional termination sequence that is functional in said plant host.

Yet another embodiment of the invention comprises the production of trehalose in a plant host due to the presence in said plant host of a

5 plant expressible gene which comprises in sequence:

(a) a transcriptional initiation region that is functional in said plant host,

(b) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally

10 (c) a transcriptional termination sequence that is functional in said plant host,

and a plant expressible gene comprising in sequence:

(d) a transcriptional initiation region that is functional in said plant host,

15 (e) a DNA sequence encoding an RNA sequence at least partially complementary to an RNA sequence which encodes a sucrose phosphate synthase enzyme naturally occurring in said plant host, and optionally

(f) a transcriptional termination sequence that is functional in said plant host,

20 and a plant expressible gene comprising in sequence:

(g) a transcriptional initiation region that is functional in said plant host,

(h) a DNA sequence encoding an RNA sequence at least partially complementary to an RNA sequence which encodes an ADP-glucose

25 pyrophosphorylase enzyme naturally occurring in said plant host, and optionally

(i) a transcriptional termination sequence that is functional in said plant host.

The invention also extends to the plant expressible genes used in  
30 the process for making trehalose, as well as to the combinations of plant expressible genes, as well as to cloning plasmids, transformation vectors, microorganisms, an individual plant cells harboring plant expressible genes according to the invention.

The invention also provides a recombinant plant DNA genome which  
35 contains a plant expressible trehalose phosphate synthase gene that is not naturally present therein. The invention also comprises a recombinant

plant DNA genome which comprises a plant expressible trehalose phosphate synthase gene that is not naturally present therein and in addition a plant expressible gene capable of inhibiting biosynthesis of an SPS activity, and/or a plant expressible gene capable of inhibiting

5 biosynthesis of an AGPase activity.

The invention also provides a method for obtaining a plant capable of producing trehalose comprising the steps of,

- (1) introducing into a recipient plant cell a plant expressible gene comprising in sequence:
- 10 (a) a transcriptional initiation region that is functional in said plant host,
- (b) a DNA sequence encoding a trehalose phosphate synthase activity,
- (c) a transcriptional termination sequence that is functional in said plant host, and a plant expressible gene comprising in sequence:
- 15 (d) a transcriptional initiation region that is functional in said plant host,
- (e) a DNA sequence encoding a selectable marker gene that is functional in said plant host, and optionally
- (f) a transcriptional termination sequence that is functional in said
- 20 plant host,
- (2) generating a plant from a transformed cell under conditions that allow for selection for the presence of the selectable marker gene.

The invention also comprises plants which produce (increased levels of) trehalose as a result of genetic modification.

25 The invention further comprises plants having a recombinant DNA genome containing a plant expressible gene according to the invention.

The invention also comprises plants having a recombinant DNA genome containing a plant expressible gene according to the invention and which plants produce trehalose.

30 The invention also comprises plants having a recombinant DNA genome according to the invention and which exhibit increased drought resistance.

The invention also extends to parts of plants according to the invention such as cells or protoplasts or cultures thereof, flowers,

35 fruits, leaves, pollen, roots (including hairy root cultures), seeds, stalks, tubers (including so-called microtubers) and the like.

The invention also extends to a method of preserving plants or plant parts in the presence of trehalose comprising the steps of:

- (1) growing a plant according to the invention which produces trehalose,
- (2) harvesting the plant or plant parts which contain trehalose, and
- 5 (3) air drying the plants or plant parts or alternatively,
- (4) freeze drying the plants or plant parts.

The invention further comprises the plants and plant parts which have been preserved by a method according to the invention.

The invention also includes a method for the production of  
10 trehalose comprising the steps of:

- (1) growing a plant which by virtue of a recombinant plant DNA genome is capable of producing (increased levels of) trehalose,
- (2) harvesting said plant or plant part,
- (3) isolating the trehalose from the said plant or the said plant part.

15 The invention further includes a method for the production of trehalose comprising the steps of:

- (1) growing in culture plant cells which by virtue of a recombinant plant DNA genome are capable of producing (increased levels of) trehalose,
- (2) isolating the trehalose from the said plant cell culture.

20 The invention further provides an isolated nucleic acid sequence encoding a trehalose phosphate synthase activity. A preferred isolated nucleic acid sequence is one obtained from E. coli, still more preferred is the isolated nucleic acid sequence represented in SEQIDNO: 2. Another preferred embodiment comprises a nucleic acid sequence that codes for an  
25 amino acid sequence as in SEQIDNO: 3.

The following figures further illustrate the invention.

#### DESCRIPTION OF THE FIGURES

Figure 1. Schematic representation of parts of the sucrose and starch  
30 biosynthetic pathways in plant sink tissues. The figure shows that carbohydrate produced in the leaf by photosynthesis is transported via the phloem tissue in the form of sucrose. Upon entering the sink it is unloaded by a membrane bound invertase activity to yield the monosugars glucose and fructose. By the action of a number of enzymatic steps these  
35 monosugars are converted to starch and/or sucrose as roughly shown here. The glucose metabolites G6P and UDPG are believed to be used as the



substrates for the TPS-enzyme engineered into the plant by introduction of the plant expressible otsA gene. The figure shows how the amount of UDPG and G6P available as substrate is increased by reducing the levels of the enzymes SPS and AGPase. Their inhibition is marked with a cross.

5

Figure 2. Schematic map of the EMBL4clone 7F11 from Kohara et al. (1987), containing the otsBA operon from E. coli. The 18.8 kb insert has been shaded. The restriction sites for the enzymes EcoRV and HindIII used to clone the otsA gene are indicated, as well as their distance in kb with respect to the left-hand site of the insert. The otsA and B gene are indicated, the arrows shows the direction of transcription. (See Fig. 8, extended map).

Figure 3. Sequence of the cloned potato SPS cDNA. Underscore: maize SPS cDNA sequences used as oligonucleotides in the PCR amplification reaction.

Figure 4. Schematic representation of binary vector pMOG664.

Figure 5. Restriction map of part of pTiB6 showing two fragments cloned in pMOG579.

20 Figure 6. Schematic representation of pMOG579 used for constructing the helper plasmid without T-region in Agrobacterium strain MOG101.

Figure 7. Schematic representation of expression vector pMOG180.

Figure 8. Extended map of the EMBL4clone 7F11 from Kohara et al. (1987), containing the otsBA operon from E. coli. The location of the TPS open reading frame (ORF) is indicated. (\*: HindIII sites not present in the map of Kohara et al., *infra*)

Figure 9. Schematic representation of binary vector pMOG799.

Figure 10. Schematic representation of binary vector pMOG801.

Figure 11. Schematic representation of binary vector pMOG802.

30

#### DETAILED DESCRIPTION OF THE INVENTION

A preferred embodiment of the invention comprises a potato plant capable of producing trehalose in tubers due to the presence in said potato plant of a plant expressible gene which comprises in

35 sequence:

(a) a transcriptional initiation region derived from the 35S RNA of CaMV

flanked upstream by a double enhancer,

(b) a DNA sequence encoding trehalose phosphate synthase which is the coding region of the otsA gene located in the otsBA operon of E. coli,

(c) a transcriptional termination sequence derived from the nopaline synthase (nos) gene of Agrobacterium. Tubers of transgenic plants containing the plant expressible TPS gene produced trehalose, whereas control plants lacking this gene did not. Apparently, the trehalose phosphate which is produced by the transgenic tubers is converted into trehalose. Apparently, it is not required to provide for a trehalose phosphate phosphatase activity since it seems present in potato.

Also illustrated in figure 1 is an approach to improve substrate availability for TPS. To this end two genes influencing the availability of glucose-6 phosphate (G6P) and UDPG, to with an antisense SPS gene and a antisense APGase have been cloned under the control of the CaMV 35S promoter for expression in plant hosts. If introduced into a plant host containing a plant expressible TPS gene according to the invention, this will increase substrate availability for TPS and therefore trehalose synthesis. It will readily occur to someone skilled in the art that also other antisense genes may be used to block the synthesis of sucrose or starch, in order to improve substrate availability.

Although the invention is described in detail for potato plants which express a plant expressible trehalose phosphate synthase gene from E. coli under the control of the CaMV 35S promoter as transcription initiation region, it will be clear to those of skill in the art that other spermatophytic plant hosts are equally suitable for the production of trehalose. Preferred plant hosts among the spermatophyta are the Angiospermae, notably the Dicotyledoneae, comprising inter alia the Solanaceae as a representative family, and the Monocotyledoneae, comprising inter alia the Gramineae as a representative family. Suitable host plants, as defined in the context of the present invention include plants (as well as parts and cells of said plants) and their progeny which have been genetically modified using recombinant DNA techniques to cause or enhance production of trehalose interest in the desired plant or plant organ; these plants may be used directly (e.g. the plant species which produce edible parts) or after the trehalose is

- purified from said host (which be from edible as well as inedible plant hosts). Crops with edible parts according to the invention include those which have flowers such as cauliflower (Brassica oleracea), artichoke (Cynara scolymus), fruits such as apple (Malus, e.g. domestica), banana
- 5 (Musa, e.g. acuminata), berries (such as the currant, Ribes, e.g. rubrum), cherries (such as the sweet cherry, Prunus, e.g. avium), cucumber (Cucumis, e.g. sativus), grape (Vitis, e.g. vinifera), lemon (Citrus limon), melon (Cucumis melo), nuts (such as the walnut, Juglans, e.g. regia; peanut, Arachis hypogaea), orange (Citrus, e.g. maxima),
- 10 peach (Prunus, e.g. persica), pear (Pyrus, e.g. communis), pepper (Solanum, e.g. capsicum), plum (Prunus, e.g. domestica), strawberry (Fragaria, e.g. moschata), tomato (Lycopersicon, e.g. esculentum), leafs, such as alfalfa (Medicago sativa), cabbages (such as Brassica oleracea), endive (Cichorium, e.g. endivia), leek (Allium porrum), lettuce (Lactuca
- 15 sativa), spinach (Spinacia oleracea), tobacco (Nicotiana tabacum), roots, such as arrowroot (Maranta arundinacea), beet (Beta vulgaris), carrot (Daucus carota), cassava (Manihot esculenta), turnip (Brassica rapa), radish (Raphanus sativus), yam (Dioscorea esculenta), sweet potato (Ipomoea batatas) and seeds, such as bean (Phaseolus vulgaris), pea
- 20 (Pisum sativum), soybean (Glycin max), wheat (Triticum aestivum), barley (Hordeum vulgare), corn (Zea mays), rice (Oryza sativa), tubers, such as kohlrabi (Brassica oleracea), potato (Solanum tuberosum), and the like. The edible parts may be conserved by drying in the presence of enhanced trehalose levels produced therein due to the presence of a plant
- 25 expressible trehalose phosphate synthase gene. It may be advantageous to produce enhanced levels of trehalose, by putting the DNA encoding the TPS activity under the control of a plant-organ or tissue-specific promoter; the choice of which can readily be determined by those of skill in the art.
- 30 Any trehalose phosphate synthase gene under the control of regulatory elements necessary for expression of DNA in plant cells, either specifically or constitutively, may be used, as long as it is capable of producing an active trehalose phosphate synthase activity. The nucleic acid sequence represented in SEQIDNO: 2, in fact any open reading
- 35 frame encoding a trehalose phosphate synthase activity according to the invention, may be altered without necessarily altering the amino acid

sequence of the protein encoded thereby. This fact is caused by the degeneracy of the genetic code. Thus the open reading frame encoding the trehalose phosphate synthase activity may be adapted to codon usage in the host plant of choice.

5           Also the isolated nucleic acid sequence represented by SEQIDNO: 2, may be used to identify trehalose phosphate synthase activities in other organisms and subsequently isolating them, by hybridising DNA from other sources with a DNA- or RNA fragment obtainable from the E. coli gene. Preferably, such DNA sequences are screened by  
10 hybridising under stringent conditions (such as temperature and ionic strength of the hybridisation mixture). Whether or not conditions are stringent also depends on the nature of the hybridisation, i.e. DNA:DNA, DNA:RNA, RNA:RNA, as well as the length of the shortest hybridising fragment. Those of skill in the art are readily capable of establishing a  
15 stringent hybridisation regime.

Sources for isolating trehalose phosphate synthase activities include microorganisms (e.g. bacteria, yeast, fungi), plants, animals, and the like. Isolated DNA sequences encoding trehalose phosphate activity from other sources may be used likewise in a method for  
20 producing trehalose according to the invention.

The invention also encompasses nucleic acid sequences which have been obtained by modifying the nucleic acid sequence represented in SEQIDNO: 2 by mutating one or more codons so that it results in amino acid changes in the encoded protein, as long as mutation of the amino  
25 acid sequence does not entirely abolish trehalose phosphate synthase activity.

In principle any plant host is suitable in combination with any plant expressible trehalose phosphate synthase gene. As trehalose genes from other sources become available these can be used in a similar  
30 way to obtain a plant expressible trehalose phosphate synthase gene combination as described here.

The inhibition of endogenous genes in order to enhance substrate availability for the trehalose phosphate synthase, as exemplified herein with the inhibition of endogenous sucrose phosphate  
35 synthase gene and the ADP-Glucose pyrophosphorylase gene, may be conducted in a number of ways the choice of which is not critical to the

invention. Preferably gene inhibition is achieved through the so-called 'antisense approach'. Herein a DNA sequence is expressed which produces an RNA that is at least partially complementary to the RNA which encodes the enzymatic activity that is to be blocked (e.g. AGP-ase or SPS, in the examples). It is preferred to use homologous antisense genes as these are more efficient than heterologous genes. The isolation of an antisense SPS gene from potato using a maize SPS-gene sequence as probe serves to illustrate the feasibility of this strategy. It is not meant to indicate that, for practicing the invention the use of homologous antisense fragments is required. An alternative method to block the synthesis of undesired enzymatic activities is the introduction into the genome of the plant host of an additional copy of an endogenous gene present in the plant host. It is often observed that such an additional copy of a gene silences the endogenous gene: this effect is referred to in the literature as the co-suppressive effect, or co-suppression.

In principle both dicotyledonous and monocotyledonous plants that are amenable for transformation, can be modified by introducing a plant expressible gene according to the invention into a recipient cell and growing a new plant that harbors and expresses the plant expressible gene. Preferred plants according to the invention are those that are capable of converting trehalose-phosphate into trehalose, and which do contain no or little trehalose degrading activity. It will be understood that plants that lack the ability to convert the trehalose phosphate into trehalose are also included in the present invention. These plants may be further modified by introducing additional genes that encode phosphatases that are capable of the conversion of trehalose phosphate into trehalose. In principle also plants are envisaged that contain trehalases, since these plants can be made suitable for the production of trehalose by inhibiting the activity of such enzymes, for instance by inhibiting expression of the genes encoding such enzymes using the antisense approach.

The method of introducing the plant expressible trehalose-phosphate synthase gene into a recipient plant cell is not crucial, as long as the gene is stably incorporated into the genome of said plant cell. In addition to the use of strains of the genus Agrobacterium various other techniques are available for the introduction of DNA into

plant cells, such as transformation of protoplasts using the calcium/polyethylene glycol method, electroporation and microinjection or (coated) particle bombardment (Potrykus, 1990, Bio/Technol. 8, 535-542).

In addition to these so-called direct DNA transformation methods, transformation systems involving vectors are widely available, such as viral vectors (e.g. from the Cauliflower Mosaic Virus (CaMV) and bacterial vectors (e.g. from the genus Agrobacterium) (Potrykus, 1990, Bio/Technol. 8, 535-542). After selection and/or screening, the protoplasts, cells or plant parts that have been transformed can be regenerated into whole plants, using methods known in the art (Horsch et al., 1985, Science 225, 1229-1231).

It has been shown that monocotyledonous plants are amenable to transformation and that fertile transgenic plants can be regenerated from transformed cells. The development of reproducible tissue culture systems for these crops, together with the powerful methods for introduction of genetic material into plant cells has facilitated transformation. Presently, preferred methods for transformation of monocots are microprojectile bombardment of explants or suspension cells, and direct DNA uptake or electroporation (Shimamoto, et al., 1989, Nature 338, 274-276). Transgenic maize plants have been obtained by introducing the Streptomyces hygroscopicus bar-gene, which encodes phosphinothricin acetyltransferase (an enzyme which inactivates the herbicide phosphinothricin), into embryogenic cells of a maize suspension culture by microprojectile bombardment (Gordon-Kamm, 1990, Plant Cell, 2, 603-618). The introduction of genetic material into aleurone protoplasts of other monocot crops such as wheat and barley has been reported (Lee, 1989, Plant Mol. Biol. 13, 21-30). Wheat plants have been regenerated from embryogenic suspension culture by selecting only the aged compact and nodular embryogenic callus tissues for the establishment of the embryogenic suspension cultures (Vasil, 1990 Bio/Technol. 8, 429-434). The combination with transformation systems for these crops enables the application of the present invention to monocots. These methods may also be applied for the transformation and regeneration of dicots.

Monocotyledonous plants, including commercially important crops such as corn are amenable to DNA transfer by Agrobacterium strains

(European patent 159 418 B1; Gould J, Michael D, Hasegawa O, Ulian EC, Peterson G, Smith RH, (1991) Plant. Physiol. 95, 426-434).

As regards the choice of the host plant it is preferred to select plant species with little or no trehalose degrading activity.

- 5 However, plants that do exhibit trehalase activity are not excluded from being a suitable host plant for the production of trehalose, although it may be necessary to provide for inhibition of trehalase activity if this prevents the accumulation of trehalose altogether. Such inhibition can be achieved using the antisense approach well known in the art, and  
10 illustrated for other purposes in this specification.

- It should also be understood that the invention is not limited to the use of the CaMV 35S promoter as transcription initiation region. Suitable DNA sequences for control of expression of the plant  
15 expressible genes, including marker genes, such as transcriptional initiation regions, enhancers, non-transcribed leaders and the like, may be derived from any gene that is expressed in a plant cell which, such as endogenous plant genes, genes naturally expressed in plant cells such as those located on wild-type T-DNA of Agrobacterium, genes of plant  
20 viruses, as well as other eukaryotic genes that include a transcription initiation region that conforms to the consensus sequence for eukaryotic transcription initiation. Also intended are hybrid promoters combining functional portions of various promoters, or synthetic equivalents thereof. Apart from constitutive promoters, inducible promoters, or  
25 promoters otherwise regulated in their expression pattern, e.g. developmentally or cell-type specific, may be used to control expression of the plant expressible genes according to the invention as long as they are expressed in plant parts that contain substrate for TPS.

- To select or screen for transformed cells, it is preferred to  
30 include a marker gene linked to the plant expressible gene according to the invention to be transferred to a plant cell. The choice of a suitable marker gene in plant transformation is well within the scope of the average skilled worker; some examples of routinely used marker genes are the neomycin phosphotransferase genes conferring resistance to kanamycin  
35 (EP-B 131 623), the Glutathion-S-transferase gene from rat liver conferring resistance to glutathione derived herbicides (EP-A 256 223),

glutamine synthetase conferring upon overexpression resistance to glutamine synthetase inhibitors such as phosphinothricin (WO87/05327), the acetyl transferase gene from Streptomyces viridochromogenes conferring resistance to the selective agent phosphinothricin (EP-A 275 957), the gene encoding a 5-enolshikimate-3-phosphate synthase (EPSPS) conferring tolerance to N-phosphonomethylglycine, the bar gene conferring resistance against Bialaphos (e.g. WO91/02071) and the like. The actual choice of the marker is not crucial as long as it is functional (i.e. selective) in combination with the plant cells of choice.

10

The marker gene and the gene of interest do not have to be linked, since co-transformation of unlinked genes (U.S. Patent 4,399,216) is also an efficient process in plant transformation.

Preferred plant material for transformation, especially for dicotyledonous crops are leaf-discs which can be readily transformed and have good regenerative capability (Horsch R.B. et al., (1985) Science 227, 1229-1231).

Whereas the production of trehalose can be achieved with the plant expressible trehalose phosphate synthase gene as the sole carbohydrate modifying gene, the invention is further illustrated with examples of additional plant expressible antisense genes that are capable of effecting an increase of the availability of the substrate for trehalose phosphate synthase. Specific examples of such genes are the plant expressible antisense genes for SPS from maize and potato and AGPase from potato. The down regulation of carbohydrate modifying enzymes using the antisense approach is not limited by the specific examples. For instance partially complementary plant expressible antisense genes can be used to inhibit expression of a target gene, as long as the plant expressible antisense gene produces a transcript that is sufficiently complementary with the transcript of the target gene and sufficiently long to inhibit expression said target gene.

It is immaterial to the invention how the presence of two or more genes in the same plant is effected. This can inter alia done be achieved by one of the following methods:

(a) transformation of the plant line with a multigene construct containing more than one gene to be introduced,



(b) co-transforming different constructs to the same plant line simultaneously,

(c) subsequent rounds of transformation of the same plant with the genes to be introduced,

- 5 (d) crossing two plants each of which contains a different gene to be introduced into the same plant.

The field of application of the invention lies both in agriculture and horticulture, for instance due to improved properties of the modified plants as such, as well as in any form of industry where  
10 trehalose is or will be applied. Trehalose phosphate and trehalose can be used as such for instance in purified form or in admixtures, or in the form of a storage product in plant parts. Plant parts harboring (increased levels of) trehalose phosphate or trehalose may be used as such or processed without the need to add trehalose.

15 Also trehalose can be purified from the plants or plant parts producing it and subsequently used in an industrial process. In the food industries trehalose can be employed by adding trehalose to foods before drying. Drying of foods is an important method of preservation in the industry. Trehalose seems especially useful to conserve food products  
20 through conventional air-drying, and to allow for fast reconstitution upon addition of water of a high quality product (Roser et al, July 1991, Trends in Food Science and Technology, pp. 166-169). The benefits include retention of natural flavors/fragrances, taste of fresh product, and nutritional value (proteins and vitamins). It has been shown that  
25 trehalose has the ability to stabilize proteins and membranes, and to form a chemically inert, stable glass. The low water activity of such thoroughly dried food products prevents chemical reactions, that could cause spoilage.

Field crops like corn, cassava, potato, sugar beet and  
30 sugarcane have since long been used as a natural source for bulk carbohydrate production (starches and sucrose). The production of trehalose in such crops, facilitated by genetic engineering of the trehalose-biosynthetic pathway into these plant species, would allow the exploitation of such engineered crops for trehalose production.

35 All references cited in this specification are indicative of the level of skill in the arts to which the invention pertains. All

publications, whether patents or otherwise, referred to previously or later in this specification are herein incorporated by reference as if each of them was individually incorporated by reference.

The Examples given below are just given for purposes of enablement and do not intend in any way to limit the scope of the invention.

## EXPERIMENTAL

### DNA manipulations

10 All DNA procedures (DNA isolation from E.coli, restriction, ligation, transformation, etc.) are performed according to standard protocols (Sambrook et al. (1989) Molecular Cloning: a laboratory manual, 2nd ed. Cold Spring Harbor Laboratory Press, CSH, New York).

### 15 Strains

In all examples E.coli K-12 strain DH5 $\alpha$  is used for cloning. The *Agrobacterium tumefaciens* strain used for plant transformation experiments is MOG101 which is a non-oncogenic octopine type helper strain derived from LBA1010 (Koekman et al. (1982) Plasmid 7, 119) by  
20 substitution of the T-DNA by a spectinomycin resistance marker.

### Construction of Agrobacterium strain MOG101

A binary vector system (Hoekema A., Hirsch, P.R., Hooykaas, P.J.J., and Schilperoort, R.A. (1983) Nature 303, 179) is used to  
25 transfer gene constructs into potato and tobacco plants. The helper plasmid conferring the *Agrobacterium tumefaciens* virulence functions is derived from the octopine Ti-plasmid pTiB6. MOG101 is an *Agrobacterium tumefaciens* strain carrying a non-oncogenic Ti-plasmid (Koekman et al. 1982, *supra*) from which the entire T-region is deleted and substituted by  
30 a bacterial Spectinomycin resistance marker from transposon Tn1831 (Hooykaas et al., 1980 Plasmid 4, 64-75).

The Ti-plasmid pTiB6 contains two adjacent T-regions, TL (T-left) and TR (T-right). To obtain a derivative lacking the TL- and TR-regions, we constructed intermediate vector pMOG579. Plasmid pMOG579  
35 is a pBR322 derivative which contains 2 Ti-plasmid fragments homologous to the fragments located left and right outside the T-regions of pTiB6

(shaded in figures 5 and 6). The 2 fragments are separated in pMOG579 by a 2.5 kb BamHI - HindIII fragment from transposon Tn1831 (Hooykaas et al., 1980 Plasmid 4, 64-75) carrying the spectinomycin resistance marker (Figure 6). The plasmid is introduced into Agrobacterium tumefaciens strain LBA1010 [C58-C9 (pTiB6) = a cured C58 strain in which pTiB6 is introduced (Koekman et al. (1982), supra), by triparental mating from E. coli, using HB101 8pRK2013 as a helper. Transconjugants are selected for resistance to Rifampicin (20 mg/l) and spectinomycin (250 mg/l). A double recombination between pMOG579 and pTiB6 resulted in loss of carbenicillin resistance (the pBR322 marker) and deletion of the entire T-region. Of 5000 spectinomycin resistant transconjugants replica plated onto carbenicillin (100 mg/l) 2 are found sensitive. Southern analysis (not shown) showed that a double crossing over event had deleted the entire T-region. The resulting strain is called MOG101. This strain and its construction is analogous to strain GV2260 (Deblaere et al. 1985, Nucl. Acid Res. 13, 4777-4788).

An alternative helper strain for MOG101 is e.g. LBA4404; this strain can also suitably be used for introduction of a binary plasmid, such as pMOG799 and subsequent plant transformation. Other suitable helper strains are readily available.

#### Construction of the expression vector pMOG180

The expression vector pMOG180 is a derivative of pMOG18 (EP 0 479 359 A1, Example 2b) wherein the gene coding for GUS is removed and other genes can be inserted between the ALMV RNA4 leader and 3' nos terminator as a BamHI fragment.

For this purpose, the EcoRI/NcoI fragment from pMOG18, containing the 35S promoter and ALMV RNA4 leader sequences is synthesized using PCR technology with the primer sets 5' GTTTCTACAGGACGGAGGATCCTGGAAGTATTTGAAAGA 3' and 5' CAGCTATGACCATGATTACG 3' thus mutating the NcoI site into a BamHI site. pMOG18 vector is then cut with EcoRI and BamHI after which the newly synthesized EcoRI/BamHI fragment can be ligated between these restriction sites. To circumvent PCR-induced random mutations in the promoter sequences, the EcoRI/EcoRV fragment in the PCR synthesized EcoRI/BamHI fragment is replaced by

wildtype sequences from pMOG18. The short EcoRV/BamHI is checked for mutations by sequencing. The resulting expression vector is plasmid pMOG180 (Figure 7).

5 Triparental matings

The binary vectors are mobilized in triparental matings with the E. coli strain HB101 containing plasmid pRK2013 (Ditta G., Stanfield, S., Corbin, D., and Helinski, D.R. et al. (1980) Proc. Natl. Acad. Sci. USA 77, 7347) into Agrobacterium tumefaciens strain MOG101 and used for transformation.

10 Transformation of tobacco (Nicotiana tabacum SR1)

Tobacco is transformed by cocultivation of plant tissue with Agrobacterium tumefaciens strain MOG101 (Hoekema et al. 1983, Nature 303, 179-180) containing the binary vector of interest as described.

Transformation is carried out using cocultivation of tobacco (Nicotiana tabacum cv. Petit Havana SR1) leaf disks as described by Horsch et al. 1985, Science 227, 1229-1231). Transgenic plants are regenerated from shoots that grow on selection medium containing either kanamycin or hygromycin, depending on the resistance gene present in the binary plasmid, rooted and transferred to soil.

20

Transformation of potato

Potato (Solanum tuberosum cv. Désiree) is transformed with the Agrobacterium tumefaciens strain MOG101 containing the binary vector of interest as described (Hoekema A., Huisman, M.J., Molendijk, L., Van den Elzen, P.J.M., and Cornelissen, B.J.C. (1989) Bio/technology 7, 273). The basic culture medium is MS30R30, consisting of MS-medium (Murashige, T., and Skoog, F. (1962) Physiol. Plan. 14, 473), supplemented with 30 g/L sucrose, R3 vitamins (Ooms et al. G., Burrell, M.M., Karp, A., Bevan, M., and Hille, J. (1987) Theor. Appl. Genet. 73, 744), 5  $\mu$ M zeatin riboside (ZR), and 0.3  $\mu$ M indole acetic acid (IAA). The media are solidified where necessary, with 0.7 g/L Daichin agar.

Tubers of Solanum tuberosum cv. Désiree are peeled and surface sterilized for 20 minutes in 0.6% hypochlorite solution containing 0.1% Tween-20. The potatoes are washed thoroughly in large volumes of sterile water for at least 2 hours. Discs of approximately 2 mm thickness are sliced from cylinders of tuber tissue prepared with a corkbore. Discs are incubated

for 20 minutes in a suspension consisting of the MS30R3 medium without ZR and IAA, containing  $10^6$ - $10^7$  bacteria/ml of Agrobacterium MOG101 containing the binary vector. The discs are subsequently blotted dry on sterile filter paper and transferred to solid MS30R3 medium with ZR and IAA. Discs are transferred to fresh medium with 100 mg/L cefotaxim and 50 mg/L vancomycin after 2 days. A week later, the discs are transferred again to the same medium, but this time with 100 mg/L kanamycin to select for transgenic shoots. After 4-8 weeks, shoots emerging from the discs are excised and placed onto rooting medium (MS30R3-medium without ZR and IAA, but with 100 mg/L cefotaxim and 100 mg/L kanamycin). The shoots are propagated axenically by meristem cuttings and transferred to soil after root development. Where appropriate, 10 mg/L hygromycin is used for selection instead of 100 mg/L kanamycin.

Transformation of potato cv. Kardal was performed essentially as for cv. Désiree, except for the following modifications:  
phytohormones in basic culture medium: zeatin riboside 3.5 mg/l;  
IAA (indole acetic acid) 0.03 mg/l. The Agrobacterium suspension used in the transformation contains  $10^5$  to  $10^6$  bacteria per milliliter. The concentration of kanamycin in the rooting medium was 50 mg/l.

20

#### Trehalose assays

Trehalose is determined essentially as described by Hottiger et al. (Hottiger et al. (1987) J. Bact. 169, 5518). Potato tuber tissue is frozen in liquid nitrogen, powdered with pestle and mortar and subsequently extracted for 60 minutes at room temperature in app. 3 volumes of 500 mM trichloroacetic acid. After centrifugation the pellet is extracted once more in the same way. The combined supernatants from the two extractions are assayed for anthrone positive material (Spiro R.G. (1966) Meth. Enzymol. 8, 3). Trehalose is determined qualitatively by TLC. The extracts are deionized (Merck, Ion exchanger V) and loaded onto Silica Gel 60 plates (Merck). After chromatography plates are developed with n-butanol-pyridine-water (15:3:2, v/v). Spots are visualized by spraying with 5 mg/ml vanillin in concentrated  $H_2SO_4$  and heating at 130°C. Commercially available trehalose (Sigma) is used as a standard.

35

Alternatively, trehalose was determined quantitatively by anion exchange

chromatography with pulsed amperometric detection. Extracts were prepared by adding 1 ml boiling water to 1 g frozen material which was subsequently heated for 15' at 100°C. Samples (25 µl) were analysed on a Dionex DX-300 liquid chromatograph equipped with a 4 x 250 mm Dionex 35391 carbopac PA-1 column and a 4 x 50 mm Dionex 43096 carbopac PA-1 precolumn. Elution was with 100 mM NaOH at 1 ml/min. Sugars were detected with a pulsed amperometric detector (Dionex, PAD-2). Commercially available trehalose (Sigma) was used as a standard.

#### 10 Enzyme assays

In all determinations non-transgenic tuber material or non-transgenic tobacco material was used as a control. Protein content in all samples is determined as described by Bradford (Bradford (1976) Anal. Biochem. 72, 248). For assays on tuber extracts, frozen potato tuber slices of app. 15 100 mg are homogenized in 100 µl 20 mM HEPES pH 7.4, centrifuged (Eppendorf, 5 minutes at maximum speed). The supernatant is used for activity assays.

SPS activity - SPS activity was determined essentially as described by 20 Amir, J. and Preiss, J. (1982). Plant Physiol. 69, 1027-1030). By changing the composition of the reaction-mixture, two different forms of activity of SPS can be determined;  $V_{max}$  and  $V_{sel}$ . The  $V_{max}$  reaction-mixture contained 3.2 mM UDP-glucose, 81 µM [ $^{14}C$ ]-UDP-glucose, 3.2 mM fructose-6-phosphate, 16 mM glucose-6-phosphate, 100 mM Hepes pH 7.4, 20 25 mM  $MgCl_2$  and 5 mM EDTA in a total volume of 50 µl. In the  $V_{sel}$  reaction-mixture, the concentration of fructose-6-phosphate and glucose-6-phosphate is halved and 5 mM inorganic phosphate is added. As a control, SPS activity is measured in the  $V_{max}$  reaction mixture without fructose-6-phosphate and glucose-6-phosphate. The reaction is carried out at room 30 temperature for 30' and stopped by heating the mixture for 5' at 95°C. The products of the reaction are treated with alkaline phosphatase and the resulting [ $^{14}C$ ]-sucrose is separated from the substrates by ion exchange chromatography. The amount of radiolabeled sucrose formed in the reaction is-measured in a scintillation-counter.

35

- TPS activity - TPS activity was measured in a similar way as described for SPS. After ion exchange chromatography the samples contained dephosphorylated sucrose as well as trehalose. To determine which proportion of the formed products is trehalose, samples were separated by
- 5 TLC as described. The extracts were deionized (Merck, Ion exchanger V) and loaded onto Silica Gel 60 plates (Merck). After chromatography, spots containing [ $^{14}\text{C}$ ]-sucrose and [ $^{14}\text{C}$ ]-trehalose were scraped off and measured in a scintillation-counter.
- 10 AGPase activity - AGPase activity is determined as described by Müller-Röber et al. (Müller-Röber B., Sonnewald, U., and Willmitzer, L. (1992) EMBO J. 11, 1229). Production of glucose-1-phosphate from ADP-glucose is determined in a NAD-linked glucose-6-phosphate dehydrogenase system. The reaction assay contained 80 mM HEPES pH 7.4, 10
- 15 mM  $\text{MgCl}_2$ , 1 mM ADP-glucose, 0.6 mM NAD, 10  $\mu\text{M}$  glucose-1,6-diphosphate, 3 mM DTT, 0.02% bovine serum albumin, 1 U phosphoglucomutase from rabbit muscle (Sigma), 2.5 U NAD-linked glucose-6-phosphate dehydrogenase from Leuconostoc mesenteroides and tuber extract. The reaction is initiated by addition of sodiumpyrophosphate to a final concentration of 2 mM. NAD
- 20 reduction is measured spectrophotometrically at 340 nm and 30°C. A unit of AGPase activity is defined as nmol glucose-1-phosphate generated per min at 30°C.

#### Example I

25 Cloning of a full length *E. coli* otsA gene

- In *E. coli* trehalose phosphate synthase (TPS) is encoded by the otsA gene located in the operon otsBA. The location and the direction of transcription of this operon on the *E. coli* chromosome are known (Kaasen, I., Falkenberg, P., Styrvold, O.B., and Ström, A.R. (1992) J.
- 30 Bact. 174, 889). The otsA gene is located at 42', and according to Kaasen et al. confined on a 18.8 kb fragment present in the EMBL4 genomic clone designated 7F11 of the map by Kohara et al. (Kohara, Y., Akiyama, K., and Isono, K. (1987) Cell 50, 495). DNA prepared from a lysate of lambda clone 7F11, and digested with HindIII. The isolated 2.9 kb HindIII
- 35 fragment (the 'right-hand' HindIII site at 14.3 kb in the insert was omitted on the map by Kohara et al., as already noticed by Kaasen et al.)

is cloned in pUC18 linearized with HindIII. The 2.9 kb HindIII insert from the resulting plasmid, designated pMOG674, is sequenced. The sequence is found to contain part of the araH gene of the arabinose transport operon (Scripture, J.B., Voelker, C., Miller, S., O'Donnell, R.T., Polgar, L., Rade, J., Horazdovsky, B.F., and Hogg, R.W. (1987) J. Mol. Biol. 197, 37), the otsB gene encoding TPP as localized by Kaasen et al. and part of the otsA gene encoding TPS. The otsA is found not to be confined to the 2.9 kb HindIII fragment as described by Kaasen et al. To complete the sequence an overlapping BamHI/EcoRI fragment is isolated and partially sequenced. The complete TPS-encoding sequence of the otsA gene is shown in SEQIDNO: 2. The position of the otsA gene on clone 7F11, with the restriction enzyme sites used, is shown in Figure 8. An additional HindIII site not present on the map published by Kohara et al. is found on the 'left-hand' site of the 2.9 kb HindIII fragment.

The HindIII site in pMOG180 is replaced by a SstI site, by cloning the oligonucleotide duplex:

SstI

5'	AGCTCACGAGCTCTCAGG	3'	(SEQIDNO: 8)
3'	GTGCTCGAGAGTCCTCGA	5'	(SEQIDNO: 9)

into pMOG180 cut with HindIII. The resulting vector is designated pMOG746. The oligonucleotide duplex:

BamHI	SmaI	SphI	HindIII	BamHI

5'	GATCCCCCGGGGCATGCAAGCTTG	3'	(SEQIDNO: 10)
3'	GGGGCCCCGTACGTTTCGAACCTAG	5'	(SEQIDNO: 11)

is cloned in vector pMOG746 linearized with BamHI. The vector with the oligonucleotide duplex in the desired orientation (checked by restriction enzyme digestion) is designated pMOG747. The 2.9 kb HindIII fragment of plasmid pMOG674 is cloned in pMOG747 linearized with HindIII, resulting in vector pMOG748. The app. 2.4 kb EcoRV/SstI and the app. 3.5 kb SstI/SmaI fragments of pMOG748 are isolated, ligated and transformed into *E. coli*, thus deleting the 3' end of the 2.9 kb HindIII fragment. The resulting plasmid is designated pMOG749. The 5' end of the otsA gene is synthesized by PCR using the synthetic oligonucleotides TPS1 and TPS2



with pMOG749 as a template.

TPS1            5'   GAGAAAATACCCGGGGTGATGAC   3'            (SEQIDNO: 12)

TPS2            5'   GATAATCGTGGATCCAGATAATGTC   3'            (SEQIDNO: 13)

5

By sequencing it is confirmed that the 0.4 kb PCR fragment has the correct sequence. The 1 kb BamHI/HindIII fragment of pMOG749 is cloned together with the 0.4 kb XmaI/BamHI PCR fragment in pMOG747 linearized with XmaI and HindIII. In the resulting plasmid, digested with HindIII and SstI, the synthetic oligonucleotide duplex TPS6/7 is cloned, encoding the three C-terminal amino acids of TPS.

LysLeuAlaStop

TPS 6/7: 5' AGCTGGCGTGAGGAGCGGTAAATAAGCTTGAGCT 3'

15 3' CCGCACTCCTCGCCAATTATTCGAAC 5'

In the resulting plasmid, digested with HindIII and SstI, the 0.25 kb HindIII/SstI fragment of plasmid pMOG749 is cloned, comprising the terminator from the Agrobacterium tumefaciens nopaline synthase (NOS) gene, resulting in plasmid pMOG798. This plasmid contains the E. coli otsA gene in the correct orientation under control of the Cauliflower Mosaic Virus (CaMV) 35S promoter with double enhancer (Guilley et al. (1982) Cell 30, 763), the Alfalfa Mosaic Virus (AMV) RNA4 leader sequence (Brederode et al. (1980) Nucl. Acids Res. 8, 2213) and the nopaline synthase transcription terminator sequence from Agrobacterium tumefaciens. The entire expression cassette is cloned as a 2.5 kb EcoRI/SstI fragment into the binary vector pMOG23 linearized with EcoRI and SstI. The resulting binary vector, pMOG799 (Fig. 9), is used to transform potato and tobacco (An E. coli strain harbouring pMOG799 has been deposited at the Centraal Bureau voor Schimmelcultures, Phabagen collections, Padualaan 8, Utrecht, The Netherlands, on August 23, 1993, deposit number CBS 430.93; pMOG23 has been deposited at the CBS on June 29, 1990, deposit number CBS 102.90).

35

### Example II

Trehalose production in tobacco transformed with pMOG799

Tobacco leaf discs are transformed with the binary vector pMOG799 using Agrobacterium tumefaciens. A number of 20 independent transgenic shoots are analysed for trehalose phosphate synthase (TPS) activity. Some tobacco plants grown in vitro were found to have extremely thick roots compared to untransformed plants. Analysis of the roots of those transgenic tobacco plants show elevated levels of trehalose in comparison with non-transgenic control plants.

### Example III

#### 10 Trehalose production in potatoes transformed with pMOG799

Potato tuber discs are transformed with the binary vector pMOG799 using Agrobacterium tumefaciens. Transgenic shoots are selected on kanamycin. A number of 20 independent transgenic shoots are analyzed for trehalose phosphate synthase (TPS) activity. Shoots found to contain the enzyme are grown to mature plants. Analyses of mature tubers of those transgenic potato plants show elevated levels of trehalose in comparison with non-transgenic control plants. Transgenic plant line MOG799.1 is propagated for further work.

### 20 Example IV

#### Construction of pMOG664

Two oligonucleotides corresponding to the cDNA sequence of the small subunit of ADP-glucose pyrophosphorylase (AGPaseB) from potato tuber cv. Désiree (Müller-Röber, B., Kossmann, J., Hannah, L.C., Willmitzer, L., and Sonnewald, U. (1990) Mol. Gen. Genet. 224, 136-146) are synthesized:

5' TCCCATGGAATCAAAGCATCC 3' (SEQIDNO: 4)

5' GATTGGATCCAGGGCACGGCTG 3' (SEQIDNO: 5)

The oligonucleotides are designed to contain suitable restriction sites (BamHI and NcoI, underlined) at their termini to allow assembly in an expression cassette in an antisense orientation after digestion with these enzymes. A fragment of about 1 kb is PCR amplified with these oligonucleotides using DNA isolated from a cDNA library from potato cv. Désiree prepared from 2 month old leaf tissue (Clontech) as a template. By sequencing it is shown, that the fragment is identical with the AGPase B sequence from potato cv. Désiree (Müller-Röber, B., Kossmann, J., Hannah, L.C., Willmitzer, L., and Sonnewald, U. (1990) Mol. Gen. Genet.

224, 136-146). Following digestion with BamHI and NcoI, the fragment is cloned in pMOG18 linearized with BamHI and NcoI. From the resulting plasmid the 1.85 kb EcoRI/BamHI fragment (containing the CaMV 35S promoter, the AMV RNA4 leader and the AGPase fragment in an antisense orientation), as well as the BamHI/HindIII fragment containing the terminator from the nopaline synthase (NOS) gene from Agrobacterium tumefaciens are cloned in a three-way ligation in the binary vector pMOG22 linearized with EcoRI and HindIII. The binary vector pMOG22 contains a plant expressible HPTII gene for hygromycin selection in transgenic plants (pMOG22 has been deposited at the Centraal Bureau voor Schimmelcultures on January 29, 1990 under accession number 101.90). The resulting binary vector pMOG664 (Fig. 4) is used for potato transformation.

15

#### Example V

##### Construction of pMOG801

A set of oligonucleotides complementary to the sequence of the maize sucrose phosphate synthase (SPS) cDNA (Worrell, A.C., Bruneau, J.-M., Summerfalt, K., Boersig, M., and Voelker, T.A. (1991) Plant Cell 3, 1121) is synthesized. Their sequences are as follows:

5' CTAGGTCGTGATTCTGATACAGGTGGCCAGGTG 3' (SEQIDNO: 6)

5' CAGCATCGGCATAGTGCCCATGTATCACGTAAGGC 3' (SEQIDNO: 7)

25 These oligonucleotides are used to PCR amplify a DNA fragment of 370 bp using DNA isolated from a potato cv. Désiree cDNA library prepared from 2 months old leaf tissue (Clontech) as a template. By sequencing of this fragment it is shown, that it is homologous to the SPS sequence of maize (see Figure 3, and Worrell et al. (1991). The PCR fragment is used to screen a lambda gtl0 library of potato cv. Désiree cDNA library prepared from 2 month old leaf tissue (Clontech). The insert of one positively hybridizing clone is sequenced. The sequence of the 654 bp DNA fragment is found to be 65% identical with the corresponding part of the maize SPS sequence (Starting at nucleotide number 349 in Figure 11 in Worrell et al. (1991). The EcoRI insert of this clone is cloned in pMOG180 digested with BamHI, in a three-way ligation with the following synthetic

oligonuclotide duplex.

5' GATCGTCAGATCTAGC 3' (SEQIDNO: 14)  
3' CAGTCTAGATCGTTAA 5' (SEQIDNO: 15)

5

The plasmid, having the SPS fragment in the antisense orientation with respect to the CaMV 35S promoter, is designated pMOG787. The EcoRI/HindIII fragment of plasmid pMOG787 is cloned in a three-way ligation with a synthetic linker:

10

5' AGCTTCCCCCCCCG 3' (SEQIDNO: 16)  
3' AGGGGGGGGCTTAA 5' (SEQIDNO: 17)

15

into the binary vector pMOG22 linearized with EcoRI. The binary vector pMOG22 contains a plant expressible HPTII gene for hygromycin selection in transgenic plants (pMOG22 has been deposited at the Centraal Bureau voor Schimmelcultures on January 29, 1990 under accession number 101.90). The resulting binary vector pMOG801 (Fig. 10) is used for potato transformation.

20

#### Example VI

##### Construction of pMOG802

The EcoRI fragment of plasmid pMOG801, containing the antisense SPS expression cassette, is cloned in the binary vector pMOG664 (containing the antisense AGPase cassette), linearized with EcoRI. The resulting binary vector is called pMOG802 (Fig 11).

#### Example VII

##### Trehalose production in potato transformed with pMOG799 and pMOG664

30 Potato tuber discs of kanamycin resistant plant line MOG799.1, expressing TPS (Example IX) are transformed with the binary vector pMOG664, containing the antisense AGPase expression cassette. Transgenic shoots, selected on 10 mg/L hygromycin, are analyzed for the presence of the TPS and antisense AGPase sequences by PCR. Transgenic plants containing both  
35 are analyzed for TPS and AGPase activity.  
By analysis of transgenic tubers for AGPase activity it is shown that,

reductions in activity levels in individual transgenic lines in comparison with non-transgenic controls occur. By Northern blots it is shown, that mRNA levels for AGPase are reduced in the transgenic plants compared to those in non-transgenic control plants. Trehalose levels in  
5 tubers of transgenic potato plants, found to exhibit TPS activity, and having reduced levels of AGPase, show an increase in comparison with the levels found in tubers of transgenic plant line MOG799.1.

#### Example VIII

##### 10 Trehalose production in potato transformed with pMOG799 and pMOG801

Potato tuber discs of kanamycin resistant plant line MOG799.1, expressing TPS (Example IX) are transformed with the binary vector pMOG801, containing the antisense SPS expression cassette. Transgenic shoots, selected on 10 mg/L hygromycin, are analyzed for the presence of the TPS  
15 and antisense SPS sequences by PCR. Transgenic plants containing both are analyzed for TPS and SPS activity.

By analysis of transgenic tubers for SPS activity it is shown that reductions in activity levels in individual transgenic lines in comparison with non-transgenic controls occur. By Northern blots it is  
20 shown, that mRNA levels for SPS are reduced in the transgenic plants compared to those in non-transgenic control plants. Trehalose levels in tubers of transgenic potato plants, found to exhibit TPS activity, and having reduced levels of SPS, show an increase in comparison with the levels found in tubers of transgenic plant line MOG799.1.

25

#### Example IX

##### Trehalose production in potato transformed with pMOG799 and pMOG802

Potato tuber discs of kanamycin resistant plant line MOG799.1, expressing TPS (Example IX) are transformed with the binary vector pMOG802,  
30 containing the antisense SPS and AGPase expression cassettes. Transgenic shoots, selected on 10 mg/L hygromycin, are analyzed for the presence of the TPS, antisense AGPase and antisense SPS sequences by PCR. Transgenic plants containing all three constructs are analyzed for TPS, AGPase and SPS activity.

35 By analysis of transgenic tubers for AGPase and SPS activity it is shown, that reductions in the activity levels for both enzymes in individual

transgenic lines in comparison with non-transgenic controls occur. By Northern blots it is shown that mRNA levels for AGPase and SPS are reduced in the transgenic plants compared to those in non-transgenic control plants. Trehalose levels in tubers of transgenic potato plants, found to exhibit TPS activity, and having reduced levels of SPS, show an increase in comparison with the levels found in tubers of transgenic plant line MOG799.1.

**Deposited strains**

- 10 pMOG22; Deposit No. CBS 101.90 (page 23, lines 18-21; page 24; lines 21-23)
- pMOG23; Deposit No. CBS 102.90 (page 22, line 10)
- pMOG799; Deposit No. CBS 430.93 (page 22, line 6)

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

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(ii) TITLE OF INVENTION: PRODUCTION OF TREHALOSE IN PLANTS

(iii) NUMBER OF SEQUENCES: 17

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP93/02290

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Solanum tuberosum  
(B) STRAIN: Desiree  
(F) TISSUE TYPE: Leaf

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTAGGTCGTG ATTCTGATAC AGGTGGCCAG GTGAAGTATG TAGTAGAGCT TGCTCGAGCA 60  
CTTGCAAACA TGAAAGGAGT TCACCGAGTT GATCTCTTGA CTCGGCAGAT CACATCCCCA 120  
GAGGTTGATT CTAGCTATGG TGAGCCAATT GAGATGCTCT CATGCCCATC TGATGCTTTG 180

GCTGCTGTGG TGCCTACTAT TCGGATCCCT GCGGACCAGG TGACAAGATA TTCCAAAAGA 240  
 ATTTACATAC CAGAATTTGT TGATGGAGCA TTAAGCCACA TTGTGAATAT GGCAAGGGCT 300  
 5 ATAGGGGAGC AAGTCAATGC TGGAAAAGCA GTGTGGCCTT ACGTGATACA TGGGCACTAT 360  
 GCCGATGCTG 370

## 10 (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## 20 (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

## 25 (vii) IMMEDIATE SOURCE:

- (B) CLONE: 7F11

## (viii) POSITION IN GENOME:

- (B) MAP POSITION: 41-42'

30

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 19..1446  
 (D) OTHER INFORMATION: /product= "trehalose phosphate  
 35 synthase"  
 /gene= "otsA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40

GAGAAAATAA CAGGAGTG ATG ACT ATG AGT CGT TTA GTC GTA GTA TCT AAC 51  
 Met Thr Met Ser Arg Leu Val Val Val Ser Asn  
 1 5 10

45 CGG ATT GCA CCA CCA GAC GAG CAC GCC GCC AGT GCC GGT GGC CTT GCC 99  
 Arg Ile Ala Pro Pro Asp Glu His Ala Ala Ser Ala Gly Gly Leu Ala  
 15 20 25

GTT GGC ATA CTG GGG GCA CTG AAA GCC GCA GGC GGA CTG TGG TTT GGC 147  
 50 Val Gly Ile Leu Gly Ala Leu Lys Ala Ala Gly Gly Leu Trp Phe Gly  
 30 35 40



31

	TGG AGT GGT GAA ACA GGG AAT GAG GAT CAG CCG CTA AAA AAG GTG AAA	195
	Trp Ser Gly Glu Thr Gly Asn Glu Asp Gln Pro Leu Lys Lys Val Lys	
	45 50 55	
5	AAA GGT AAC ATT ACG TGG GCC TCT TTT AAC CTC AGC GAA CAG GAC CTT	243
	Lys Gly Asn Ile Thr Trp Ala Ser Phe Asn Leu Ser Glu Gln Asp Leu	
	60 65 70 75	
10	GAC GAA TAC TAC AAC CAA TTC TCC AAT GCC GTT CTC TGG CCC GCT TTT	291
	Asp Glu Tyr Tyr Asn Gln Phe Ser Asn Ala Val Leu Trp Pro Ala Phe	
	80 85 90	
	CAT TAT CGG CTC GAT CTG GTG CAA TTT CAG CGT CCT GCC TGG GAC GGC	339
	His Tyr Arg Leu Asp Leu Val Gln Phe Gln Arg Pro Ala Trp Asp Gly	
15	95 100 105	
	TAT CTA CGC GTA AAT GCG TTG CTG GCA GAT AAA TTA CTG CCG CTG TTG	387
	Tyr Leu Arg Val Asn Ala Leu Leu Ala Asp Lys Leu Leu Pro Leu Leu	
	110 115 120	
20	CAA GAC GAT GAC ATT ATC TGG ATC CAC GAT TAT CAC CTG TTG CCA TTT	435
	Gln Asp Asp Asp Ile Ile Trp Ile His Asp Tyr His Leu Leu Pro Phe	
	125 130 135	
25	GCG CAT GAA TTA CGC AAA CGG GGA GTG AAT AAT CGC ATT GGT TTC TTT	483
	Ala His Glu Leu Arg Lys Arg Gly Val Asn Asn Arg Ile Gly Phe Phe	
	140 145 150 155	
	CTG CAT ATT CCT TTC CCG ACA CCG GAA ATC TTC AAC GCG CTG CCG ACA	531
30	Leu His Ile Pro Phe Pro Thr Pro Glu Ile Phe Asn Ala Leu Pro Thr	
	160 165 170	
	TAT GAC ACC TTG CTT GAA CAG CTT TGT GAT TAT GAT TTG CTG GGT TTC	579
	Tyr Asp Thr Leu Leu Glu Gln Leu Cys Asp Tyr Asp Leu Leu Gly Phe	
35	175 180 185	
	CAG ACA GAA AAC GAT CGT CTG GCG TTC CTG GAT TGT CTT TCT AAC CTG	627
	Gln Thr Glu Asn Asp Arg Leu Ala Phe Leu Asp Cys Leu Ser Asn Leu	
	190 195 200	
40	ACC CGC GTC ACG ACA CGT AGC GCA AAA AGC CAT ACA GCC TGG GGC AAA	675
	Thr Arg Val Thr Thr Arg Ser Ala Lys Ser His Thr Ala Trp Gly Lys	
	205 210 215	
45	GCA TTT CGA ACA GAA GTC TAC CCG ATC GGC ATT GAA CCG AAA GAA ATA	723
	Ala Phe Arg Thr Glu Val Tyr Pro Ile Gly Ile Glu Pro Lys Glu Ile	
	220 225 230 235	
	GCC AAA CAG GCT GCC GGG CCA CTG CCG CCA AAA CTG GCG CAA CTT AAA	771
50	Ala Lys Gln Ala Ala Gly Pro Leu Pro Pro Lys Leu Ala Gln Leu Lys	
	240 245 250	

	GCG GAA CTG AAA AAC GTA CAA AAT ATC TTT TCT GTC GAA CGG CTG GAT	819
	Ala Glu Leu Lys Asn Val Gln Asn Ile Phe Ser Val Glu Arg Leu Asp	
	255 260 265	
5	TAT TCC AAA GGT TTG CCA GAG CGT TTT CTC GCC TAT GAA GCG TTG CTG	867
	Tyr Ser Lys Gly Leu Pro Glu Arg Phe Leu Ala Tyr Glu Ala Leu Leu	
	270 275 280	
	GAA AAA TAT CCG CAG CAT CAT GGT AAA ATT CGT TAT ACC CAG ATT GCA	915
10	Glu Lys Tyr Pro Gln His His Gly Lys Ile Arg Tyr Thr Gln Ile Ala	
	285 290 295	
	CCA ACG TCG CGT GGT GAT GTG CAA GCC TAT CAG GAT ATT CGT CAT CAG	963
15	Pro Thr Ser Arg Gly Asp Val Gln Ala Tyr Gln Asp Ile Arg His Gln	
	300 305 310 315	
	CTC GAA AAT GAA GCT GGA CGA ATT AAT GGT AAA TAC GGG CAA TTA GGC	1011
20	Leu Glu Asn Glu Ala Gly Arg Ile Asn Gly Lys Tyr Gly Gln Leu Gly	
	320 325 330	
	TGG ACG CCG CTT TAT TAT TTG AAT CAG CAT TTT GAC CGT AAA TTA CTG	1059
	Trp Thr Pro Leu Tyr Tyr Leu Asn Gln His Phe Asp Arg Lys Leu Leu	
	335 340 345	
25	ATG AAA ATA TTC CGC TAC TCT GAC GTG GGC TTA GTG ACG CCA CTG CGT	1107
	Met Lys Ile Phe Arg Tyr Ser Asp Val Gly Leu Val Thr Pro Leu Arg	
	350 355 360	
	GAC GGG ATG AAC CTG GTA GCA AAA GAG TAT GTT GCT GCT CAG GAC CCA	1155
30	Asp Gly Met Asn Leu Val Ala Lys Glu Tyr Val Ala Ala Gln Asp Pro	
	365 370 375	
	GCC AAT CCG GGC GTT CTT GTT CTT TCG CAA TTT GCG GGA GCG GCA AAC	1203
35	Ala Asn Pro Gly Val Leu Val Leu Ser Gln Phe Ala Gly Ala Ala Asn	
	380 385 390 395	
	GAG TTA ACG TCG GCG TTA ATT GTT AAC CCC TAC GAT CGT GAC GAA GTT	1251
40	Glu Leu Thr Ser Ala Leu Ile Val Asn Pro Tyr Asp Arg Asp Glu Val	
	400 405 410	
	GCA GCT GCG CTG GAT CGT GCA TTG ACT ATG TCG CTG GCG GAA CGT ATT	1299
	Ala Ala Ala Leu Asp Arg Ala Leu Thr Met Ser Leu Ala Glu Arg Ile	
	415 420 425	
45	TCC CGT CAT GCA GAA ATG CTG GAC GTT ATC GTG AAA AAC GAT ATT AAC	1347
	Ser Arg His Ala Glu Met Leu Asp Val Ile Val Lys Asn Asp Ile Asn	
	430 435 440	
	CAC TGG CAG GAG TGC TTC ATT AGC GAC CTA AAG CAG ATA GTT CCG CGA	1395
50	His Trp Gln Glu Cys Phe Ile Ser Asp Leu Lys Gln Ile Val Pro Arg	
	445 450 455	

AGC GCG GAA AGC CAG CAG CGC GAT AAA GTT GCT ACC TTT CCA AAG CTT 1443  
 Ser Ala Glu Ser Gln Gln Arg Asp Lys Val Ala Thr Phe Pro Lys Leu  
 460 465 470 475

5 GCG 1446  
 Ala

## 10 (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids  
 (B) TYPE: amino acid  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

20 Met Thr Met Ser Arg Leu Val Val Val Ser Asn Arg Ile Ala Pro Pro  
 1 5 10 15

25 Asp Glu His Ala Ala Ser Ala Gly Gly Leu Ala Val Gly Ile Leu Gly  
 20 25 30

Ala Leu Lys Ala Ala Gly Gly Leu Trp Phe Gly Trp Ser Gly Glu Thr  
 35 40 45

30 Gly Asn Glu Asp Gln Pro Leu Lys Lys Val Lys Lys Gly Asn Ile Thr  
 50 55 60

Trp Ala Ser Phe Asn Leu Ser Glu Gln Asp Leu Asp Glu Tyr Tyr Asn  
 65 70 75 80

35 Gln Phe Ser Asn Ala Val Leu Trp Pro Ala Phe His Tyr Arg Leu Asp  
 85 90 95

Leu Val Gln Phe Gln Arg Pro Ala Trp Asp Gly Tyr Leu Arg Val Asn  
 40 100 105 110

Ala Leu Leu Ala Asp Lys Leu Leu Pro Leu Leu Gln Asp Asp Asp Ile  
 115 120 125

45 Ile Trp Ile His Asp Tyr His Leu Leu Pro Phe Ala His Glu Leu Arg  
 130 135 140

Lys Arg Gly Val Asn Asn Arg Ile Gly Phe Phe Leu His Ile Pro Phe  
 145 150 155 160

50 -  
 Pro Thr Pro Glu Ile Phe Asn Ala Leu Pro Thr Tyr Asp Thr Leu Leu  
 165 170 175

Glu Gln Leu Cys Asp Tyr Asp Leu Leu Gly Phe Gln Thr Glu Asn Asp  
 180 185 190

5 Arg Leu Ala Phe Leu Asp Cys Leu Ser Asn Leu Thr Arg Val Thr Thr  
 195 200 205

Arg Ser Ala Lys Ser His Thr Ala Trp Gly Lys Ala Phe Arg Thr Glu  
 210 215 220

10 Val Tyr Pro Ile Gly Ile Glu Pro Lys Glu Ile Ala Lys Gln Ala Ala  
 225 230 235 240

15 Gly Pro Leu Pro Pro Lys Leu Ala Gln Leu Lys Ala Glu Leu Lys Asn  
 245 250 255

Val Gln Asn Ile Phe Ser Val Glu Arg Leu Asp Tyr Ser Lys Gly Leu  
 260 265 270

20 Pro Glu Arg Phe Leu Ala Tyr Glu Ala Leu Leu Glu Lys Tyr Pro Gln  
 275 280 285

25 His His Gly Lys Ile Arg Tyr Thr Gln Ile Ala Pro Thr Ser Arg Gly  
 290 295 300

Asp Val Gln Ala Tyr Gln Asp Ile Arg His Gln Leu Glu Asn Glu Ala  
 305 310 315 320

30 Gly Arg Ile Asn Gly Lys Tyr Gly Gln Leu Gly Trp Thr Pro Leu Tyr  
 325 330 335

Tyr Leu Asn Gln His Phe Asp Arg Lys Leu Leu Met Lys Ile Phe Arg  
 340 345 350

35 Tyr Ser Asp Val Gly Leu Val Thr Pro Leu Arg Asp Gly Met Asn Leu  
 355 360 365

Val Ala Lys Glu Tyr Val Ala Ala Gln Asp Pro Ala Asn Pro Gly Val  
 370 375 380

40 Leu Val Leu Ser Gln Phe Ala Gly Ala Ala Asn Glu Leu Thr Ser Ala  
 385 390 395 400

Leu Ile Val Asn Pro Tyr Asp Arg Asp Glu Val Ala Ala Ala Leu Asp  
 405 410 415

45 Arg Ala Leu Thr Met Ser Leu Ala Glu Arg Ile Ser Arg His Ala Glu  
 420 425 430

50 Met Leu Asp Val Ile Val Lys Asn Asp Ile Asn His Trp Gln Glu Cys  
 435 440 445

35

Phe Ile Ser Asp Leu Lys Gln Ile Val Pro Arg Ser Ala Glu Ser Gln  
450 455 460

Gln Arg Asp Lys Val Ala Thr Phe Pro Lys Leu Ala  
5 465 470 475

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

20 TCCCCATGGA ATCAAAGCAT CC 22

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

35 GATTGGATCC AGGGCACGGC TG 22

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50 (iii) HYPOTHETICAL: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

36

CTAGGTCGTG ATTCTGATAC AGGTGGCCAG GTG

33

(2) INFORMATION FOR SEQ ID NO: 7:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGCATCGGC ATAGTGCCCA TGTATCACGT AAGGC

35

20 (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

30

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AGCTCAGGAG CTCTCAGG

18

35

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

45

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

50 GTGCTCGAGA GTCCTCGA

18

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
5 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCCCCGG GGCATGCAAG CTTG

24

15

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
20 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

30 GGGGCCCCGT ACGTTCGAAC CTAG

24

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

45

GAGAAAATAC CCGGGGTGAT GAC

23

(2) INFORMATION FOR SEQ ID NO: 13:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

10 GATAATCGTG GATCCAGATA ATGTC

25

(2) INFORMATION FOR SEQ ID NO: 14:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

25

GATCGTCAGA TCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 15:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAGTCTAGAT CGTTAA

16

(2) INFORMATION FOR SEQ ID NO: 16:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA



(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

5

AGCTTCCCCC CCG

13

(2) INFORMATION FOR SEQ ID NO: 17:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AGGGGGGGCT TAA

13

## CLAIMS

1. A plant expressible gene which when expressed in a plant or plant cell increases the trehalose content of said plant or plant cell.
- 5 2. A plant expressible gene according to claim 1 which comprises in sequence:
  - (a) a transcriptional initiation region that is functional in said plant host,
  - (b) a DNA sequence encoding a trehalose phosphate synthase activity, and
  - 10 optionally
  - (c) a transcriptional termination sequence that is functional in said plant host..
3. A plant expressible gene according to claim 2, wherein the said  
15 DNA sequence encodes a trehalose phosphate synthase activity represented by the amino acid sequence of SEQIDNO: 2.
4. A plant expressible gene according to claim 2, wherein the DNA  
20 sequence encoding a trehalose phosphate synthase activity comprises the open reading frame of the otsA gene of *E. coli*.
5. A plant expressible gene according to claim 2 to 4, wherein  
said transcriptional initiation site comprises a promoter region of the  
35S RNA encoding DNA of the cauliflower mosaic virus and the  
25 transcription terminator region of the nopaline synthase gene of *Agrobacterium tumefaciens*.
6. A plant expressible gene according to claim 2, as is present in  
pMOG799, deposited at the Centraal Bureau voor Schimmelcultures,  
30 Accession No. 430.93.
7. A DNA sequence containing a plant expressible gene which  
comprises in sequence:
  - (a) a transcriptional initiation region that is functional in said plant
  - 35 host,
  - (b) a DNA sequence encoding a trehalose phosphate synthase activity, and

optionally

- (c) a transcriptional termination sequence that is functional in said plant host,
- and a plant expressible gene comprising in sequence:
  - 5 (d) a transcriptional initiation region that is functional in said plant host,
  - (e) a DNA sequence encoding an RNA sequence at least partially complementary to an RNA sequence which encodes sucrose phosphate synthase enzyme (SPS) naturally occurring in said plant host, and optionally
  - 10 (f) a transcriptional termination sequence that is functional in said plant host.

8. A DNA sequence comprising a plant expressible gene which comprises in sequence:

- 15 (a) a transcriptional initiation region that is functional in said plant host,
- (b) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally
- (c) a transcriptional termination sequence that is functional in said
- 20 plant host, and
- a plant expressible gene comprising in sequence:
  - (d) a transcriptional initiation region that is functional in said plant host,
  - (e) a DNA sequence encoding an RNA sequence at least partially
  - 25 complementary to an RNA sequence which encodes a ADP-glucose pyrophosphorylase enzyme naturally occurring in said plant host, and optionally
  - (f) a transcriptional termination sequence that is functional in said plant host.

30

9. A DNA sequence comprising a plant expressible gene which comprises in sequence:

- (a) a transcriptional initiation region that is functional in said plant host,
- 35 (b) a DNA sequence encoding a trehalose phosphate synthase activity, and optionally

(c) a transcriptional termination sequence that is functional in said plant host,

and a plant expressible gene comprising in sequence:

5 (a) a transcriptional initiation region that is functional in said plant host,

(b) a DNA sequence encoding an RNA sequence at least partially complementary to an RNA sequence which encodes a sucrose phosphate synthase enzyme naturally occurring in said plant host, and optionally

10 (c) a transcriptional termination sequence that is functional in said plant host,

and a plant expressible gene comprising in sequence:

(a) a transcriptional initiation region that is functional in said plant host,

15 (b) a DNA sequence encoding an RNA sequence at least partially complementary to an RNA sequence which encodes a ADP-glucose pyrophosphorylase enzyme naturally occurring in said plant host, and optionally

(c) a transcriptional termination sequence that is functional in said plant host.

20

10. A cloning vector which comprises a plant expressible gene according to any one of claims 1 to 6.

25 11. A cloning vector which comprises a DNA sequence of any one of the claims 7 to 9.

12. A binary vector comprising a plant expressible gene according to any one of claims 1 to 6.

30 13. A binary vector comprising a DNA sequence according to any one of claims 7 to 9.

14. A microorganism comprising a vector of any one of the claims 10 to 13.

35

15. A microorganism according to claim 12 or 13 which is of the

genus Agrobacterium.

16. A method for obtaining a plant with increased capability of producing trehalose comprising the steps of,

- 5 (1) introducing into a recipient cell of a plant a plant expressible gene which when expressed in a plant or plant cell increases the trehalose content of said plant or plant cell,  
and a plant expressible gene comprising in sequence:

- (a) a transcriptional initiation region that is functional in said plant  
10 host,  
(b) a DNA sequence encoding a selectable marker gene that is functional in said plant host, and optionally  
(c) a transcriptional termination sequence that is functional in said plant host,  
15 (2) generating a plant from a transformed cell under conditions that allow for selection for the presence of the selectable marker gene.

17. A recombinant plant DNA genome which contains a plant expressible trehalose phosphate synthase gene that is not naturally  
20 present therein.

18. A recombinant plant DNA genome which comprises  
(a) a plant expressible gene encoding trehalose phosphate synthase, and  
(b) a plant expressible gene capable of inhibiting the biosynthesis of a  
25 sucrose phosphate synthesis activity.

19. A recombinant plant DNA genome which comprises:  
(a) a plant expressible gene encoding trehalose phosphate synthase,  
(b) a plant expressible gene capable of inhibiting the biosynthesis of an  
30 ADP-Glucose pyrophosphorylase activity.

20. A recombinant plant DNA genome which comprises:  
(a) a plant expressible gene encoding trehalose phosphate synthase,  
(b) a plant expressible gene capable of inhibiting the biosynthesis of an  
35 ADP-Glucose pyrophosphorylase activity, and  
(c) a plant expressible gene capable of inhibiting the biosynthesis of an

sucrose phosphate synthesis activity.

21. A plant cell having a recombinant plant DNA genome of any one of the claims 17 to 20.

5

22. A plant cell culture comprising plant cells of claim 21.

23. A plant containing a cell of claim 21.

10 24. A plant consisting predominantly of cells according to claim 21.

25. A plant capable of producing increased levels of trehalose as a result of genetic modification.

15

26. The plant of claim 25 which contains increased levels of trehalose.

27. The plant of claim 25 which belongs to the Angiospermae.

20

28. The plant of claim 27, which is of the family *Solanaceae*.

29. The plant of claim 28, which is *Solanum tuberosum*.

25 30. A part of a plant according to any one of claims 25 to 29.

31. A part of a plant according to claim, said part containing increased levels of trehalose.

30 32. A part according to any one of the claims 30 or 31 selected from the group consisting of bulbs, flowers, fruits, hairy roots, leaves, microtubers, pollen, roots, seeds, stalks and tubers.

33. A method of preserving a plant or plant part in the presence of trehalose, comprising the steps of:

35

(1) growing a plant of any one of the claims 25 to 26, or growing a plant

part of any one of the claims 29 to 30,

- (2) harvesting the plant or the plant part which contains trehalose, and
- (3) air drying the plant or plant part or alternatively,
- (4) freeze drying the plant or plant part.

5

34. A dried plant or plant part which obtainable by the method of claim 31.

35. A method for the production of trehalose comprising the steps  
10 of:

- (1) growing a plant of claim 25 under conditions allowing for the production of trehalose,
- (2) harvesting said plant or a part thereof,
- (3) isolating the trehalose from the said plant or the said part thereof.

15

36. An isolated DNA sequence encoding a full length trehalose phosphate synthase activity.

37. An isolated DNA sequence according to claim 36, which is  
20 obtainable from E. coli.

38. An isolated DNA sequence according to claim 35 which is represented by SEQIDNO: 2.

25 39. An isolated nucleic acid sequence that codes for the amino acid sequence of SEQIDNO: 3.









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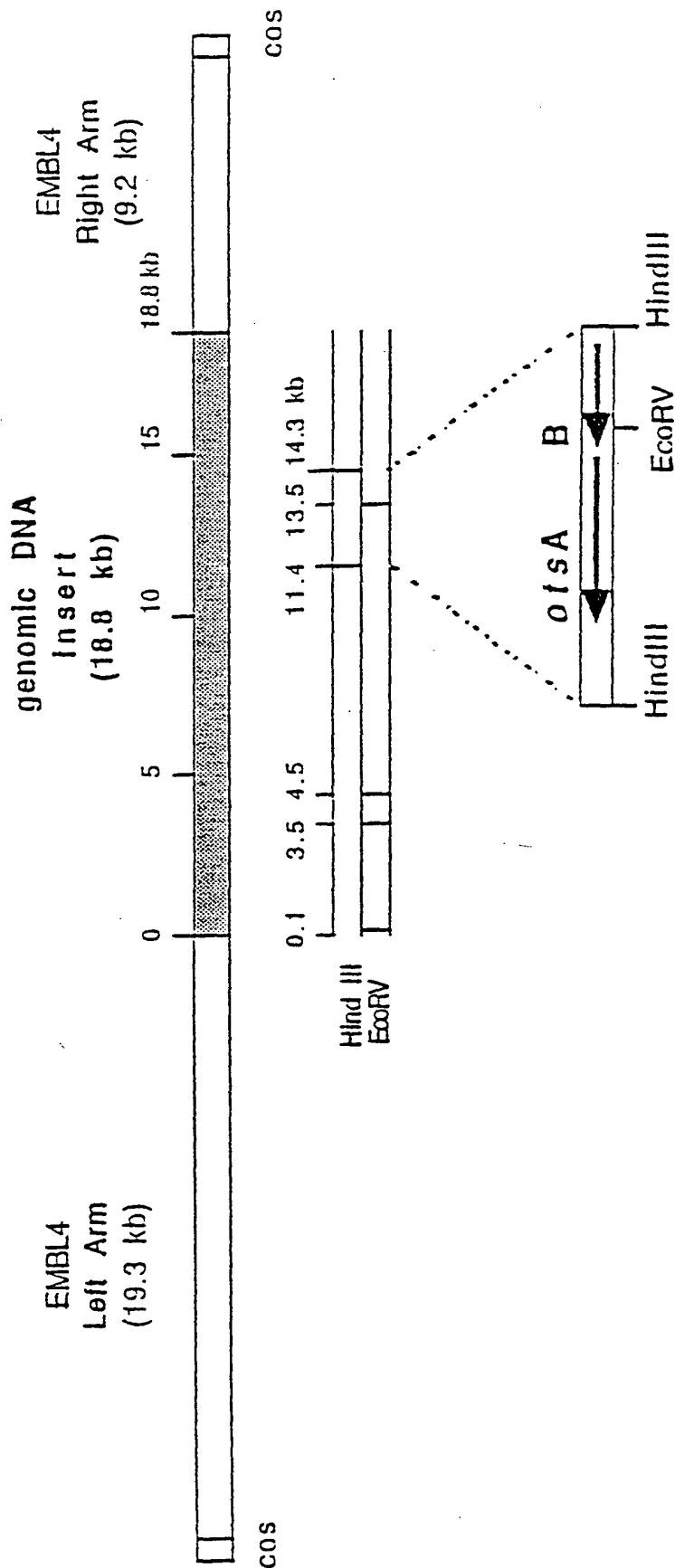


Figure 2



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1	CTAGGTCGTG	ATTCTGATAC	AGGTGGCCAG	GTGAAGTATG	TAGTAGAGCT	TGCTCGAGCA	60
61	CTTGCAACA	TGAAGGAGT	TCACCGAGTT	GATCTCTTGA	CTCGGCAGAT	CACATCCCCA	120
121	GAGGTTGATT	CTAGCTATGG	TGAGCCAATT	GAGATGCTCT	CATGCCCCATC	TGATGCTTTG	180
181	GCTGCTGTGG	TGCCCTACTAT	TCGGATCCCT	GCGGACCCAGG	TGACAAAGATA	TTCCAAAAGA	240
241	ATTACATAC	CAGAAATTGT	TGATGGAGCA	TTAAGCCACA	TGTGAATAT	GGCAAGGGCT	300
301	ATAGGGGAGC	AAGTCAATGC	TGGAAGAAGCA	GTGTGGCCTT	ACGTGATACA	TGGGCACATAT	360
361	GCCGATGCTG						370

Fig. 3



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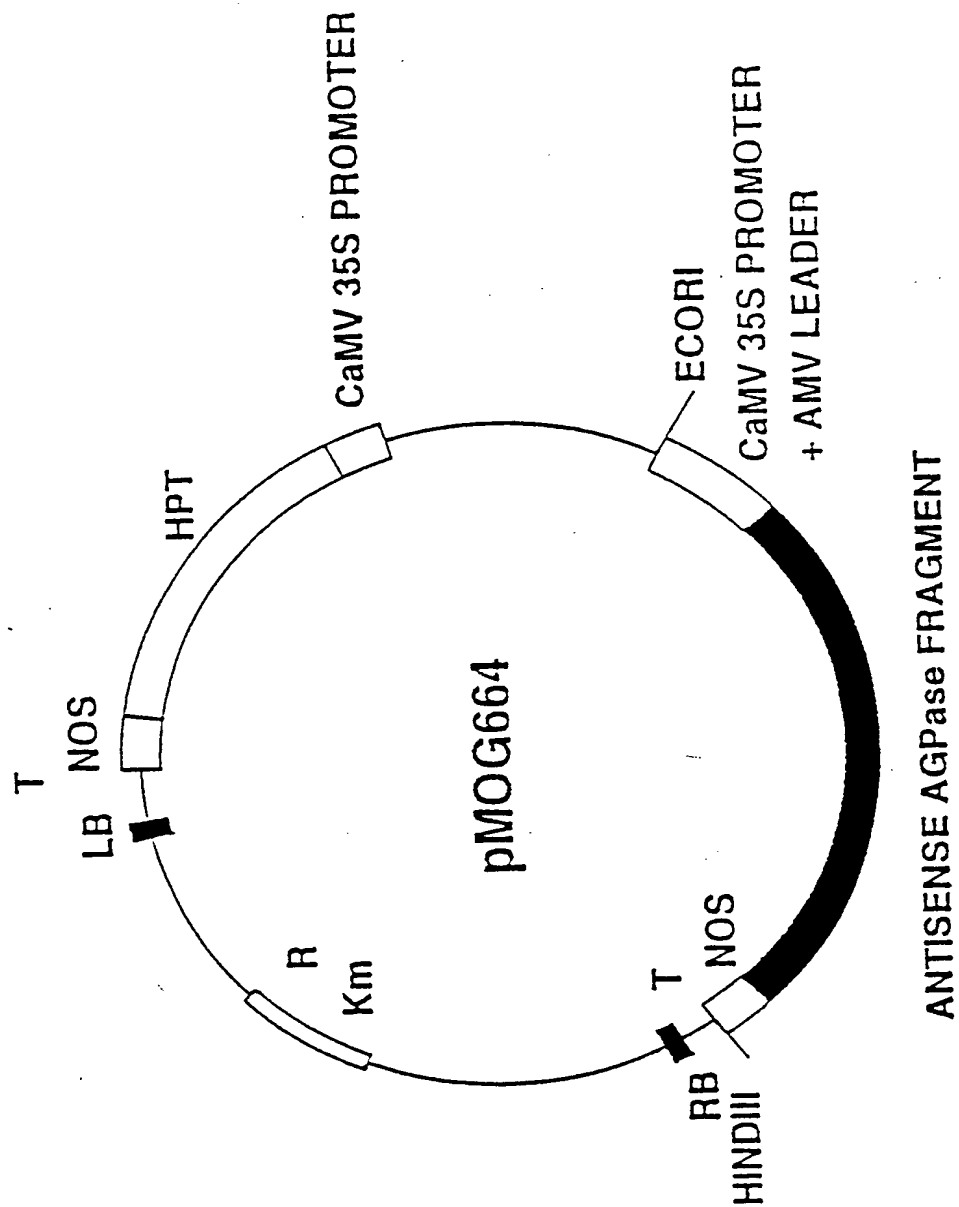


Fig. 4





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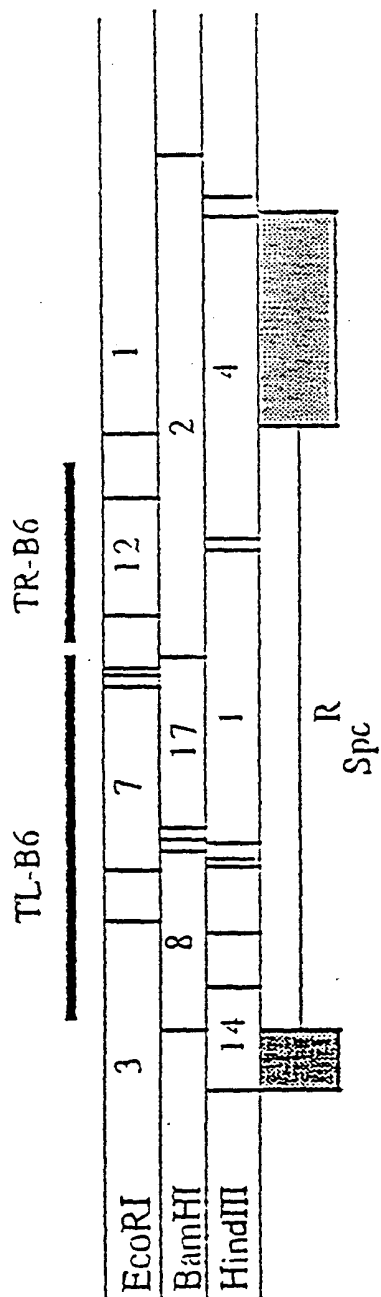
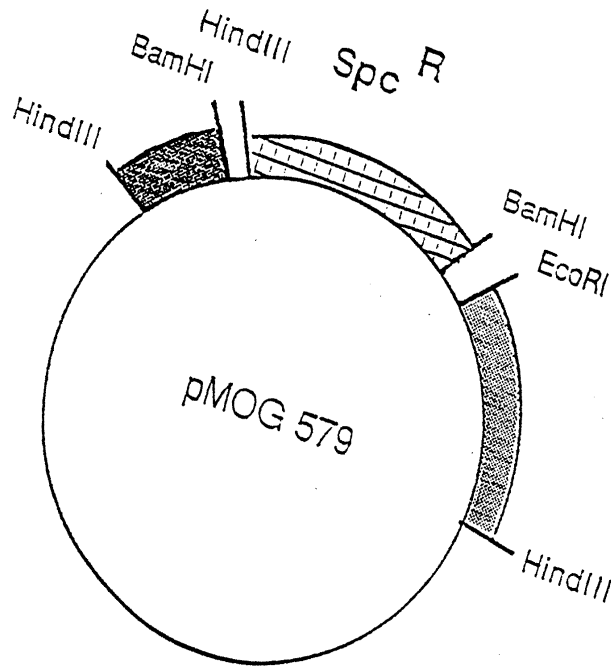


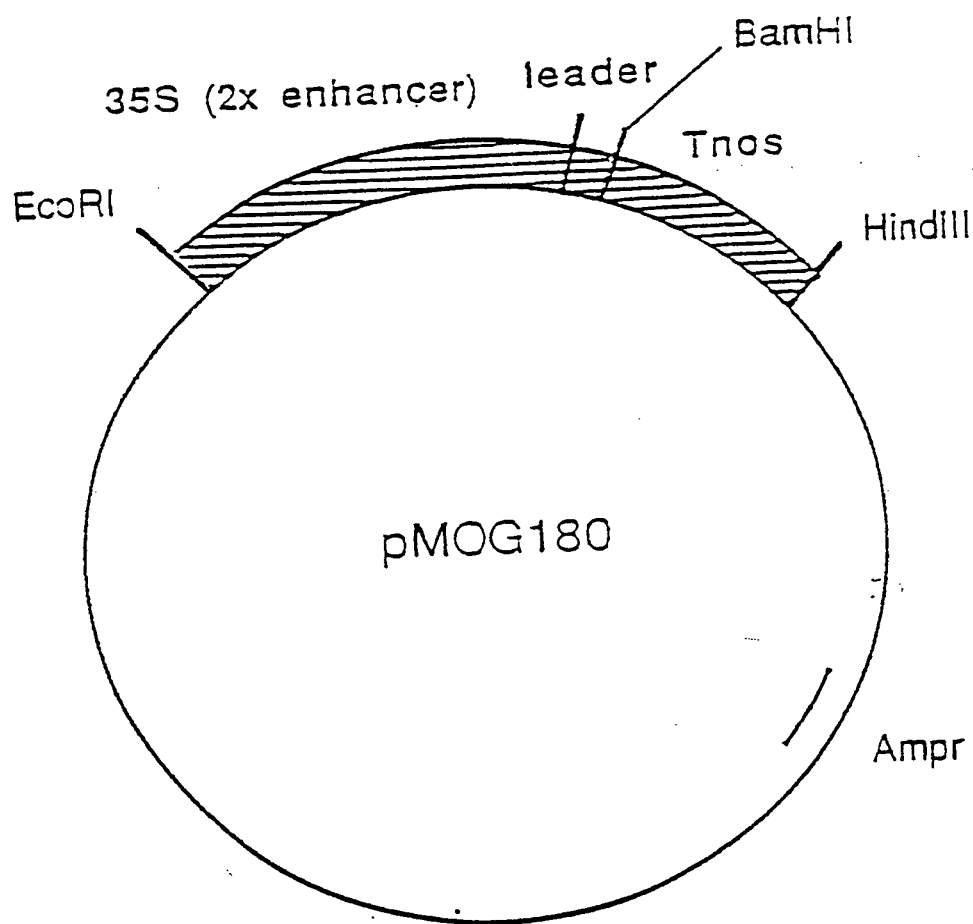
Fig. 5







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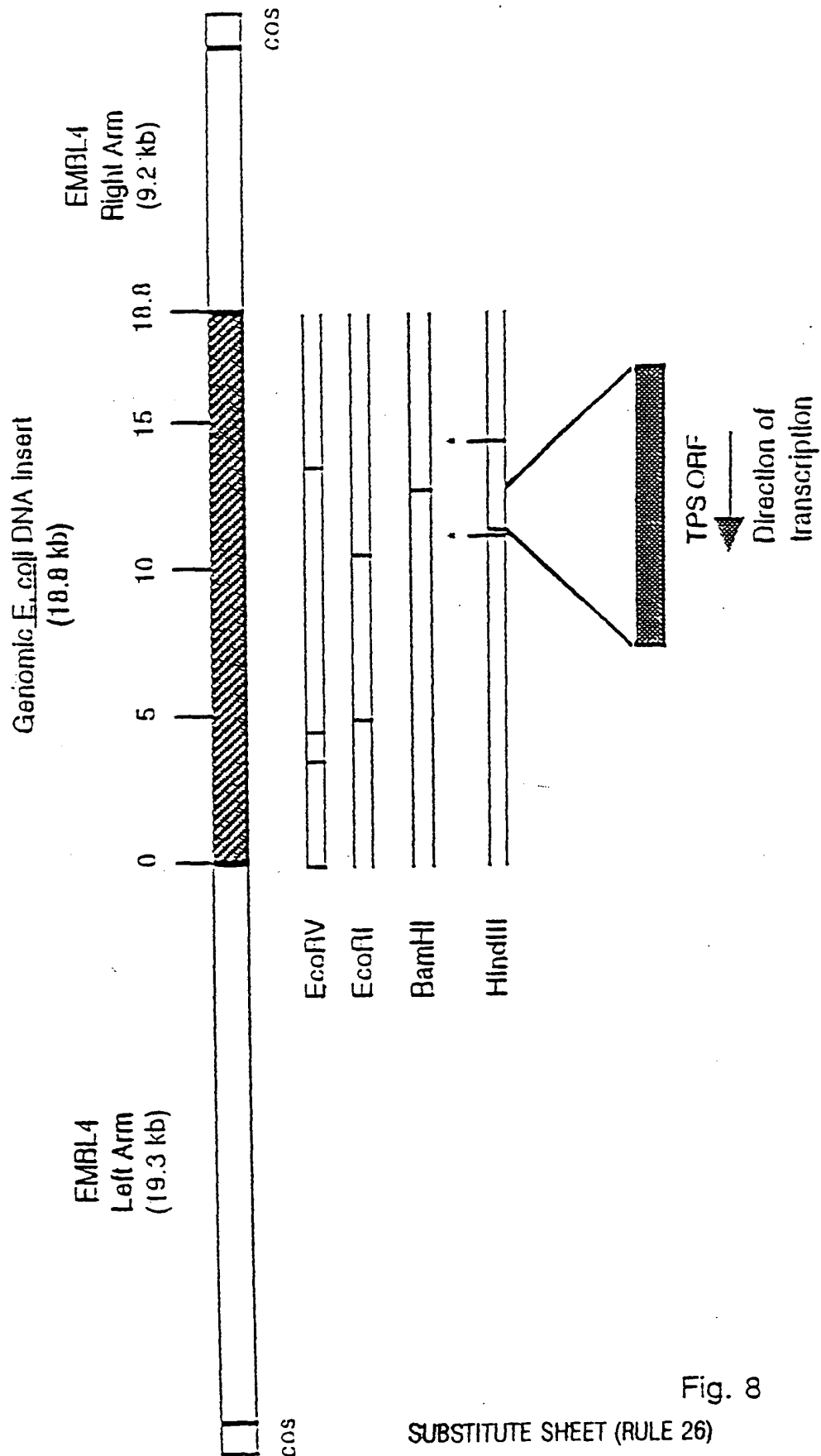


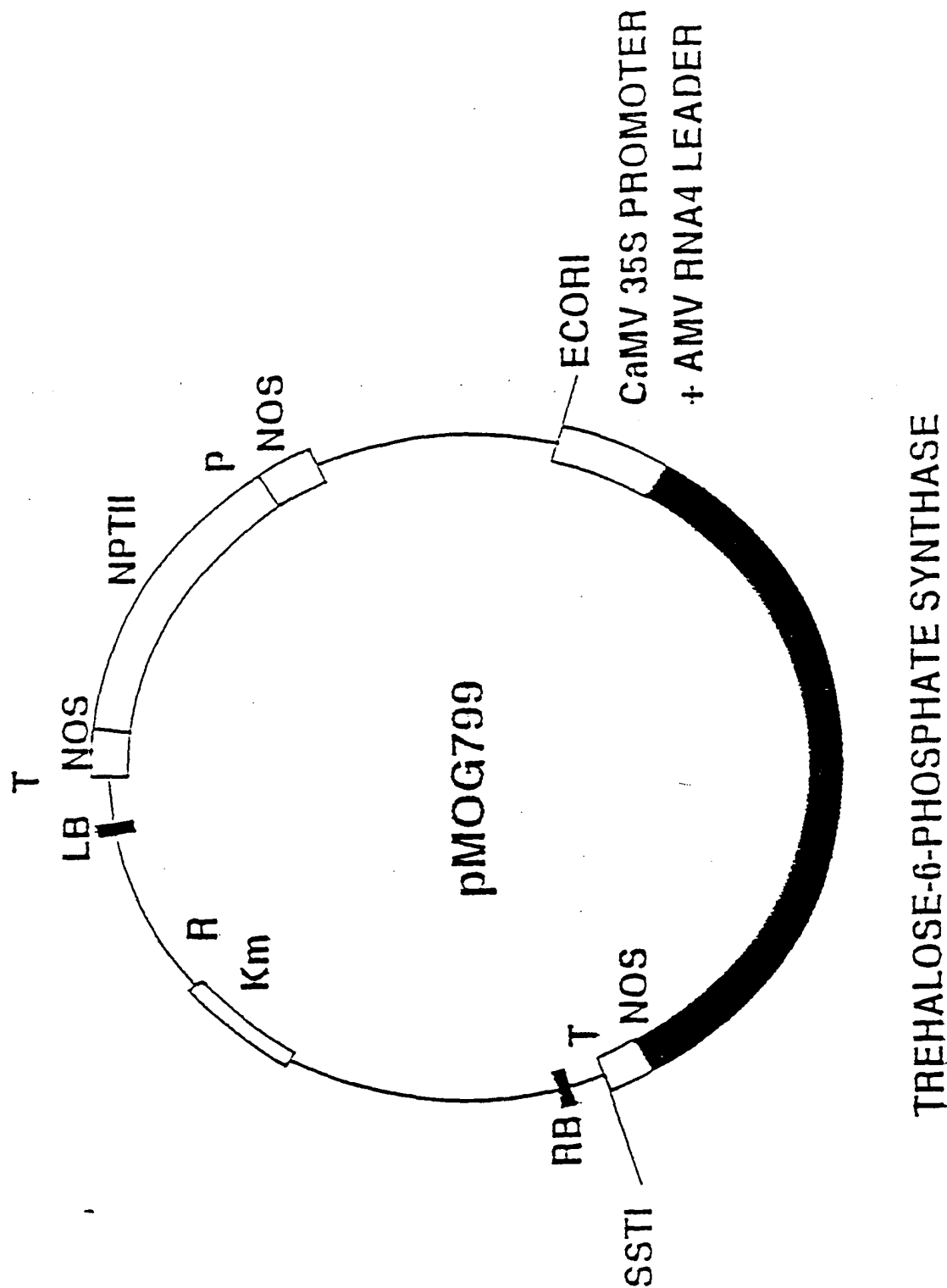
Fig. 8

SUBSTITUTE SHEET (RULE 26)





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TREHALOSE-6-PHOSPHATE SYNTHASE

Fig. 9



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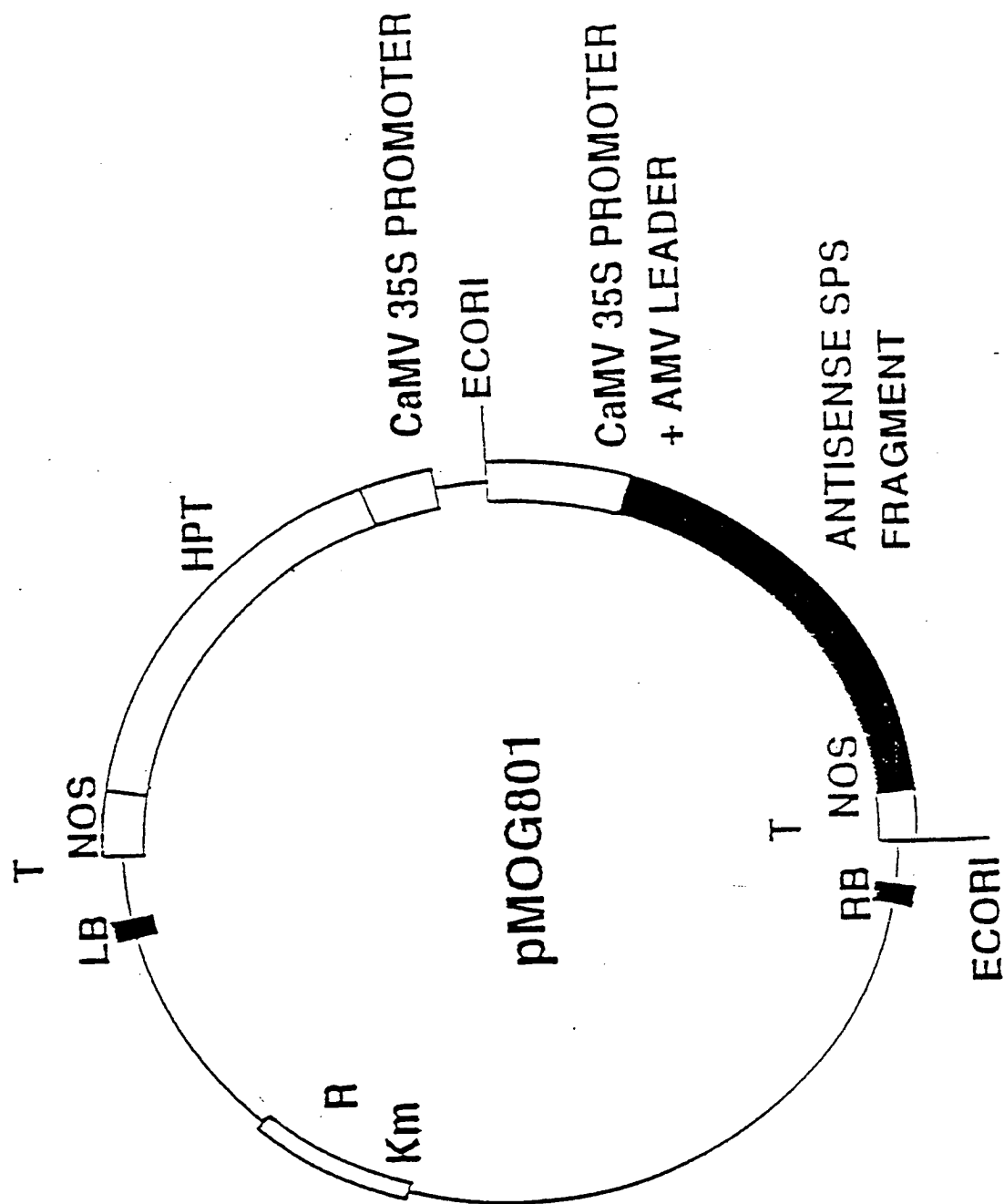


Fig. 10



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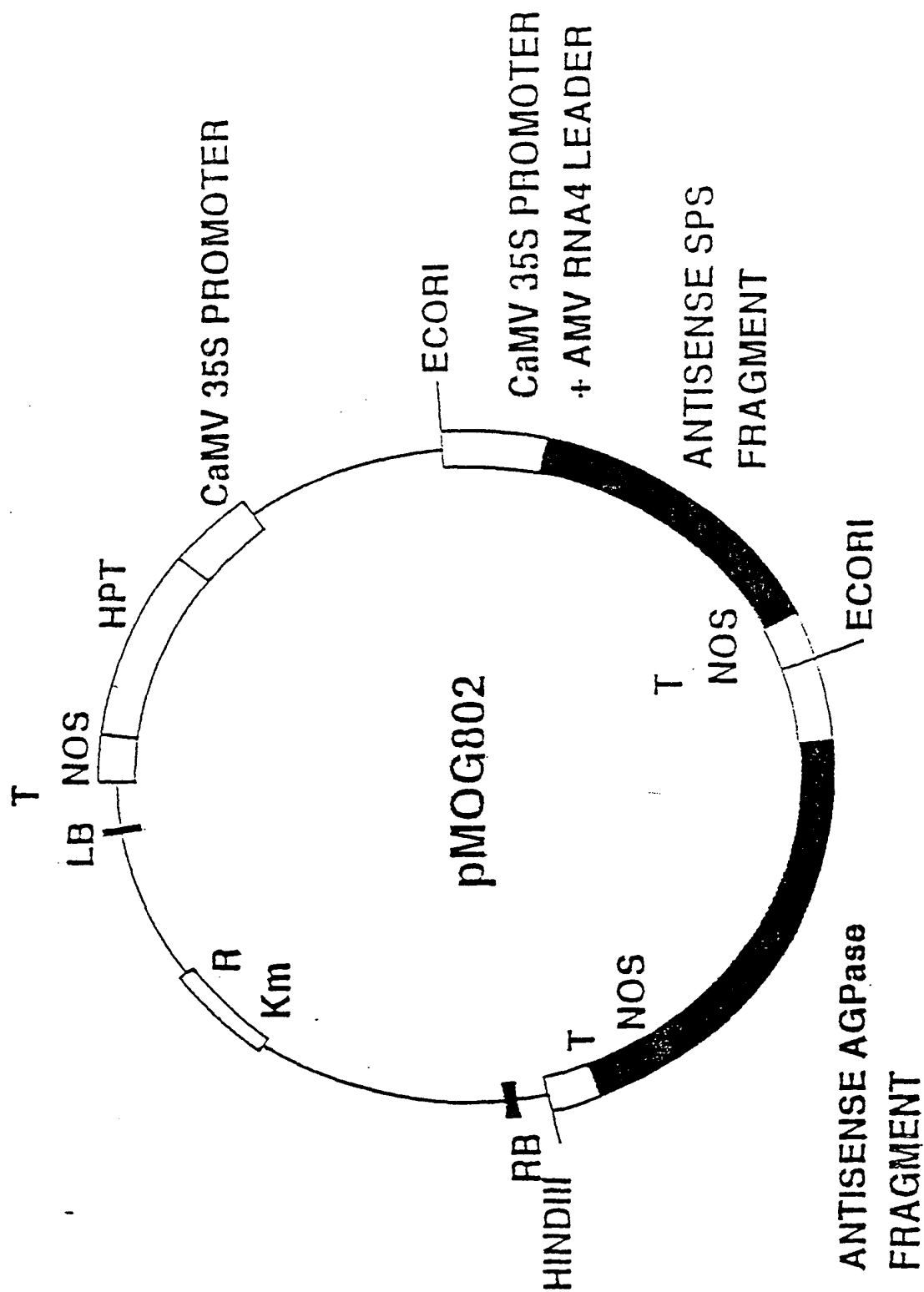


Fig. 11

